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OM protein - protein search, using SW model

Run on: June 22, 2004, 08:40:22 : Search time 34.3333 Seconds

(without alignments)
 82.295 Million cell updates/sec

Title: US-09-529-206D-4_COPY_127_136

Perfect score: 47

Sequence: 1 TVGZNLTIR 10

Scoring table: BL0SUM62

Gapep 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database :

A_Geneseq_29Jan04,*

1: GeneseqP1980s,*

2: GeneseqP1990s,*

3: GeneseqP2000s,*

4: GeneseqP2001s,*

5: GeneseqP2002s,*

6: GeneseqP2003as,*

7: GeneseqP2003bs,*

8: GeneseqP2004s,*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the scope of the distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	47	100.0	10	2	AY05980		Aay05980 Human can
2	47	100.0	10	2	AY05980		Aay05980 Human can
3	47	100.0	14	4	AEE07788		Aee07788 Human NY
4	47	100.0	14	4	AEE07728		Aee07728 Human NY
5	47	100.0	15	4	AEE07726		Aee07726 Human NY
6	47	100.0	15	4	AEE07727		Aee07727 Human NY
7	47	100.0	15	4	AEE07786		Aee07786 Human NY
8	47	100.0	15	4	AEE07787		Aee07787 Human NY
9	47	100.0	18	3	AAI52440		Aai52440 Human tum
10	47	100.0	18	4	AAB69940		Aab69940 Human NY-
11	47	100.0	18	4	AAB69944		Aab69944 Human NY-
12	47	100.0	18	4	AAU0544		Aau0544 HLA-DR53
13	47	100.0	18	4	AAB01540		Aab01540 HLA-DR53
14	47	100.0	18	4	AAB07769		Aab07769 Human NY
15	47	100.0	20	4	AAB07742		Aab07742 Human ESO
16	47	100.0	25	4	AAB07718		Aab07718 Human NY
17	47	100.0	25	7	ADD71521		Add71521 HLA-DR4 b
18	47	100.0	27	4	AAB07717		Aab07717 Human NY
19	47	100.0	30	5	AAW8510		Aaw8510 Human NY
20	47	100.0	36	5	AB679131		Abg79131 Human NY-
21	47	100.0	180	2	ABW62584		Aaw62584 Cancer as
22	47	100.0	180	2	ABW62585		Aaw62585 Human NY-
23	47	100.0	180	2	ALY05965		Aay05965 Human can
24	47	100.0	180	3	ALY52430		Aay52430 Human tum
25	47	100.0	180	3	AY070862		Aay070862 Human tum

ALIGNMENTS

RESULT 1	ID	AAV05980 standard; peptide; 10 AA.
XX	XX	
AC	AAV05980;	
XX	XX	
DT	16-AUG-1999 (first entry)	
XX	XX	
DE	Human cancer antigen NY ESO-1/CAG-3 ORF1	cancer peptide ESO10-127.
XX	XX	
KW	NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;	
KW	leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;	
KW	metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;	
KW	uterine cancer; breast cancer; prostate cancer; ovarian cancer;	
KW	cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;	
KW	liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;	
KW	vaccine.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
PN	W09918205-A2.	
XX	XX	
PD	15-APR-1999.	
XX	XX	
PF	21-SEP-1998;	9B90-US019609.
XX	XX	
PR	08-OCT-1997;	97US-0051428P.
XX	XX	
PA	US DEPT HEALTH & HUMAN SERVICES.	
XX	XX	
PI	Wang RF, Rosenberg SA;	
XX	XX	
DR	WPI; 1998-277270/23.	
XX	XX	
PT	Cancer antigen NY ESO1/CAG-3.	
XX	XX	
PS	Claim 17; Page 64; 88pp; English.	
XX	XX	
CC	This sequence represents cancer Peptide ESO10-127 that corresponds to amino acid residues 127-136 of human ESO-1/CAG-3 (or CAG-3) ORF1 (see AAY0965), a new and potent tumour antigen capable of eliciting an antigen specific immune response by T cells. Cancer peptides derived from CAG-3 ORF1, CAG-3 ORF2 (see AAY0966), portions of them and their variants (see AAY0967-87), are useful as cancer vaccines that protect against cancer. The invention provides: vectors and host cells (also transgenic animal) antisense oligonucleotides that inhibit expression of the cancer peptide or tumour antigen; antibodies reacting with a CAG-3	

cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a patient.

Sequence 10 AA;

Query Match 100.0%; Score 47; DB 2; Length 10;
Best Local Similarity 100.0%; Ptd. No. 0.0029; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 2
AY05988 AY05988 standard; peptide; 10 AA.
ID XX
AC AAY05988;
DT 16-AUG-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 HLA peptide motif.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; human leukocyte antigen; HLA;
OS Homo sapiens.
XX
PN W09918206-A2.
PD 15-APR-1999.
PP 21-SEP-1998; 98WO-US0196609.
XX
PR 08-OCT-1997; 97US-0061428P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-436851/54.

XX
PT New NY-BSO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX
Example 6; Fig 6A; 134pp; English.
XX
CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY BSO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapy strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-BSO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human NY BSO-1
CC peptide used in the characterisation of the NY BSO-1 epitope recognised
CC by T84-1.
XX
SQ Sequence 14 AA;

Query Match 100.0%; Score 47; DB 4; Length 14;
XX
Best Local Similarity 100.0%; Ptd. No. 0.0029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 3
AAE07788 AAE07788 standard; peptide; 14 AA.

ID XX
AC AAE07788;
DT 06-NOV-2001 (first entry)
XX
DB Human NY ESO-1 Peptide #22 to characterise epitope recognised by T84-1.
XX
KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW immunotherapy.

OS Homo sapiens.
XX
PN W00015393-A2.
XX
PD 02-AUG-2001.
XX
PP 26-JAN-2001; 2001WO-US002765.
XX
PR 28-JAN-2000; 2000US-0179004P.
PR 29-SEP-2000; 2000US-0237107P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Wang R, Rosenberg SA, Zeng G;
XX
DR WPI; 2001-436851/54.

XX
PT New NY-BSO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX
Example 6; Fig 6A; 134pp; English.

CC The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY BSO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapy strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-BSO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is human NY BSO-1
CC peptide used in the characterisation of the NY BSO-1 epitope recognised
CC by T84-1.
XX
SQ Sequence 14 AA;

Best Local Similarity 100.0%; Pred. No. 0.0045;
 Matches 10; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

RESULT 5
 AAE07726
 ID AAE07726 standard; peptide: 15 AA.

Qy 1 TVSGNLTIR 10
 Db 4 TVSGNLTIR 13

RESULT 4
 AAE07728
 ID AAE07728 standard; peptide; 14 AA.
 XX 06-NOV-2001 (first entry)
 XX Human NY ESO-1 MHC class II restricted T cell epitope #14.

Human; major histocompatibility complex; MHC; vaccine; metastasis;
 class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 tumour-specific humoral-mediated immunity; cancer; Cytostatic;
 immunotherapy.

XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 tumour-specific humoral-mediated immunity; cancer; Cytostatic;
 immunotherapy.
 XX Homo sapiens.
 CS WO200155393-A2.
 XX PR 02-AUG-2001.
 XX PD 26-JAN-2001; 2001WO-US0002765.
 XX PR 28-JAN-2000; 2000US-0179004P.
 XX PR 29-SEP-2000; 2000US-0237107P.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PA Wang R, Rosenberg SA, Zeng G;
 XX DR WPI; 2001-496851/54.
 XX PA New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.
 XX PS Claim 4; Page 16; 134pp; English.

XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.

XX PS Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major
 histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 restricted. The products of the gene are promising candidates for
 immunotherapeutic strategies for the prevention, treatment and diagnosis
 of patients with cancer. The cancer epitopes are useful as immunogen and
 vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 lymphocytes resulting in protection of the recipient from development of
 cancer and protection from metastasis, or by inhibiting the growth of
 cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 useful as diagnostic agent to detect the presence of cancer, to enhance
 the generation of antibody and/or T cell responses against any given
 target antigen and/or hapten and to induce tumour-specific humoral-
 mediated immunity against cancer. The present sequence is MHC class II
 restricted T cell epitope of human NY ESO-1 protein

XX Sequence 14 AA;

XX Query Match 100.0%; Score 47; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0045; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

RESULT 6

AAE07727

Db 4 TVSGNLTIR 13

RESULT 5
 AAE07726
 ID AAE07726 standard; peptide: 15 AA.

XX 06-NOV-2001 (first entry)
 XX Human NY ESO-1 MHC class II restricted T cell epitope #12.

XX Human; major histocompatibility complex; MHC; vaccine;
 metastasis; class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 tumour-specific humoral-mediated immunity; cancer; Cytostatic;
 immunotherapy.

XX Homo sapiens.
 CS WO200155393-A2.
 XX PR 02-AUG-2001.

XX PD 26-JAN-2001; 2001WO-US0002765.

XX PR 28-JAN-2000; 2000US-0179004P.

XX PR 29-SEP-2000; 2000US-0237107P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PA Wang R, Rosenberg SA, Zeng G;

XX DR WPI; 2001-496851/54.

XX PA New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.

XX PS Claim 4; Page 16; 134pp; English.

XX The invention relates to the identification and isolation of major
 histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 restricted. The products of the gene are promising candidates for
 immunotherapeutic strategies for the prevention, treatment and diagnosis
 of patients with cancer. The cancer epitopes are useful as immunogen and
 vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 lymphocytes resulting in protection of the recipient from development of
 cancer and protection from metastasis, or by inhibiting the growth of
 cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 useful as diagnostic agent to detect the presence of cancer, to enhance
 the generation of antibody and/or T cell responses against any given
 target antigen and/or hapten and to induce tumour-specific humoral-
 mediated immunity against cancer. The present sequence is MHC class II
 restricted T cell epitope of human NY ESO-1 protein

XX Sequence 15 AA;

XX Query Match 100.0%; Score 47; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.0049; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

XX Query Match 100.0%; Score 47; DB 4; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0045; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

XX AAE07727 standard; peptide; 15 AA.
 XX DE Human NY ESO-1 peptide #20 to characterise epitope recognised by TB4-1.
 XX DE Human; major histocompatibility complex; MHC; vaccine; metastasis;
 XX DT 06-NOV-2001 (first entry)
 DE Human NY ESO-1 MHC class II restricted T cell epitope #13.
 XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 XX DE Human NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 XX DE Human NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 XX DE tumour-specific humoral-mediated immunity; cancer; cytostatic;
 XX DE immunotherapy.
 XX DE Homo sapiens.
 XX DE OS Homo sapiens.
 XX DE PN WO200155393-A2.
 XX DE PD 02-AUG-2001.
 XX DE PR 26-JAN-2001; 2001WO-US002765.
 XX DE PR 28-JAN-2000; 2000US-017904P.
 XX DE PR 29-SEP-2000; 2000US-0237107P.
 XX DE PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX DE PA Wang R, Rosenberg SA, Zeng G;
 XX DE PR WPI; 2001-496851/54.
 XX DE PR New NY ESO cancer peptide or MHC class II restricted T cell epitopes,
 XX DE PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 XX DE PT protection from metastasis.
 XX DE PS Example 6; Fig 6A; 134pp; English.
 XX DE CC The invention relates to the identification and isolation of major
 XX DE CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 XX DE CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 XX DE CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 XX DE CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 XX DE CC restricted. The products of the gene are promising candidates for
 XX DE CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 XX DE CC of patients with cancer. The cancer epitopes are useful as immunogen and
 XX DE CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 XX DE CC lymphocytes resulting in protection of the recipient from development of
 XX DE CC cancer and protection from metastasis, or by inhibiting the growth of
 XX DE CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 XX DE CC useful as diagnostic agent to detect the presence of cancer, to enhance
 XX DE CC the generation of antibody and/or CD4+ T cell responses against any given
 XX DE CC target antigen and/or hapten and to induce tumour-specific humoral-
 XX DE CC mediated immunity against cancer. The present sequence is human NY ESO-1
 XX DE CC peptide used in the characterisation of the NY ESO-1 epitope recognised
 XX DE CC by TB4-1.
 XX DE SQ Sequence 15 AA;
 XX DE Query Match 100.0%; Score 47; DB 4; Length 15;
 XX DE Best Local Similarity 100.0%; Pred. No. 0.0049;
 XX DE Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX DE SQ Sequence 15 AA;
 XX DE Query Match 100.0%; Score 47; DB 4; Length 15;
 XX DE Best Local Similarity 100.0%; Pred. No. 0.0049;
 XX DE Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX DE RESULT 8
 XX DE AAE07786
 ID AAE07786 standard; peptide; 15 AA.
 XX DE Human NY ESO-1 peptide #21 to characterise epitope recognised by TE4-1.
 XX DE AC AAE07786;
 XX DE DB Human; major histocompatibility complex; MHC; vaccine; metastasis;
 XX DE DT 06-NOV-2001 (first entry)
 XX DE RESULT 7
 XX DE AAE07786
 ID AAE07786 standard; peptide; 15 AA.
 XX DE AC AAE07786;
 XX DE DB Human; major histocompatibility complex; MHC; vaccine; metastasis;

class II restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX OS Homo sapiens.

XX PN WO2001553933-A2.

XX XX PD 02-AUG-2001.

XX XX PF 26-JAN-2001; 2001WO-US002765.

XX PR 28-JAN-2000; 2000US-0179004P.

XX PR 29-SEP-2000; 2000US-0237107P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Wang R, Rosenberg SA, Zeng G;

XX DR WPI; 2001-496851/54.

XX PS Example 6; FIG 6A; 134PP; English.

PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes.

PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis.

XX PS Example 6; FIG 6A; 134PP; English.

CC The invention relates to the identification and isolation of major histocompatibility (MHC) class II restricted T cell epitope (MHC-II epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP restricted. The products of the gene are promising candidates for immunotherapeutic strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection from metastasis, or by inhibiting the growth of cells expressing the NY-ESO-1 gene product. The cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance the generation of antibody and/or CD8+ T cell responses against any given target antigen and/or hapten and to induce tumour-specific humoral-mediated immunity against cancer. The present sequence is human NY ESO-1 peptide used in the characterisation of the NY ESO-1 epitope recognised by TE4-1

CC Sequence 15 AA:

Query Match 100.0%; Score 47; DB 4; Length 15;

Best Local Similarity 100.0%; Pred. No. 0.0049;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

Db 5 TVSGNLTIR 14

RESULT 9

AY52440 ID AY52440 standard; protein: 18 AA.

XX AC AY52440;

DT 15-FEB-2000 (first entry)

XX DE Human tumour antigen NY-ESO-1 peptide #13.

XX KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II; T-cell; helper; stimulation; treatment; diagnosis;

XX prevention; melanoma; breast cancer; ovarian cancer; prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.

XX SQ Sequence 15 AA:

Query Match 100.0%; Score 47; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 0.0062;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

Db 1 TVSGNLTIR 10

RESULT 10

AAB69940 ID AAB69940 standard; peptide: 18 AA.

XX AC AAB69940;

XX DT 27-APR-2001 (first entry)

XX DB Human NY-ESO-1 HLA-DR53 binding motif #2.

XX KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;

XX KW HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;

XX KW non-small cell lung carcinoma; tumour status determination.

XX OS Homo sapiens.

XX PN WO200107917-A1.

XX XX PD 01-FEB-2001.

XX XX PF 14-JUL-2000; 2000WO-US019220.

XX XX

helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in free form is useful for this stimulation. The nucleic acid is useful for screening for a cancerous condition, which involves contacting a subject to a cell line transfected with the immunoreactive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the complex.

Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 1 TVSGNLTIR 10

RESULT 13

AAU01540 standard; peptide; 18 AA.

ID AAU01540
XX DT 18-JUL-2001 (first entry)

DE HLA-DR53 recognising NY-ESO-1 peptide #2.

XX NY-ESO-1: human; tumour rejection antigen precursor; SSX-2; MHC Class II;
KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
< KW human leukocyte antigen-determining region; disease progression;
KW disease regression; disease onset; body tissue; body fluid; enzyme label;
KW radioactive label; monoclonal antibody.
XX Homo sapiens.
OS WO200123560-A2.
PN 05-APR-2001.
XX 26-SEP-2000; 2000WO-US026411.

XX 29-SEP-1999; 99US-00008036.

XX PA (LUDWIG INST CANCER RES.

XX PI Tureci O, Sahin U, Pfreundschuh M;

DR WPI; 2001-26156/27.

XX Polypeptides binding to major histocompatibility complex class II human leukocyte antigen-determining region molecule having amino acid sequence found in tumor rejection antigen precursor used for stimulating proliferation of helper T cells.

XX Example 13; Page 19; 62pp; English.

XX The sequence represents a human NY-ESO-1 tumour rejection antigen precursor fragment which recognises and binds to HLA-DR3. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to major histocompatibility complex (MHC) Class II molecules and stimulate proliferation of helper T cells. The peptides can be administered to an HLA-DR positive subject in order to stimulate the helper T cells. An MHC Class II HLA-DR-NY-ESO-1/SSX-2 complex expressed on the surface of a cell or present in free form is useful for this stimulation. The nucleic acid is useful for

screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoreactive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the complex.

Sequence 18 AA;

Query Match 100.0%; Score 47; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 7 TVSGNLTIR 16

RESULT 14

AAB07769 standard; peptide; 18 AA.

ID AAB07769
XX AC 06-NOV-2001 (first entry)

DE Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.

XX DT 06-NOV-2001 (first entry)

DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

XX DE Human NY ESO-1 HLA DR restricted T cell epitope; MHC-II epitope; cancer antigen; NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA; tumour-specific humoral-mediated immunity; cancer; cytostatic; immunotherapy.

CC screening for a cancerous condition, which involves contacting a subject sample to a cell line transfected with the immunoreactive cell (helper T cell), where interaction is indicative of cancer. In addition, a sample from a patient (for example, a body fluid or tissue) can be monitored for the amount of the complex present in the bloodstream. This is useful for determining regression, progression or onset of a cancerous condition. The method involves contacting the sample with a radioactive labelled or enzyme labelled monoclonal antibody which specifically binds with the complex.

CC Sequence 18 AA;

CC Query Match 100.0%; Score 47; DB 4; Length 18;
CC Best Local Similarity 100.0%; Pred. No. 0.0062;
CC Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 TVSGNLTIR 10
CC Db 7 TVSGNLTIR 16

CC RESULT 14

CC ID AAB07769 standard; peptide; 18 AA.

CC AC AAB07769;
CC XX 06-NOV-2001 (first entry)

CC DE Human NY ESO-1 HLA DR restricted T cell cancer peptide #1.

CC XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
CC class II restricted T cell epitope; MHC-II epitope; cancer antigen;
CC NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
CC tumour-specific humoral-mediated immunity; cancer; cytostatic;
CC immunotherapy.

CC XX Homo sapiens.

CC OS WO200155393-A2.

CC PD 02-AUG-2001.

CC PP 26-JAN-2001; 2001WO-US002765.

CC PR 28-JAN-2000; 2000US-0179004P.

CC PR 29-SEP-2000; 2000US-0237107P.

CC PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

CC XX Wang R, Rosenberg SA, Zeng G;

CC DR WPI; 2001-496851/54.

CC PT New NY-ESO cancer Peptide or MHC class II restricted T cell epitopes, useful as immunogen and vaccine for inhibiting cancer in a mammal or as protection from metastasis.

CC Claim 84; Page 84; 134pp; English.

CC The invention relates to the identification and isolation of major MHC-II histocompatibility (MHC) class II restricted T cell epitope (epitope), derived from the cancer antigen, NY SSO-1. The MHC-II epitopes from NY SSO-1 are recognised by CD4+ T lymphocytes in an human leucocyte antigen (HLA) class II restricted manner. In Particular HLA-DR or HLA-DP restricted. The products of the gene are promising candidates for immunotherapy strategies for the prevention, treatment and diagnosis of patients with cancer. The cancer epitopes are useful as immunogen and vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T lymphocytes resulting in protection of the recipient from development of cancer and protection of the gene products or by inhibiting the growth of cells expressing the NY-ESO-1 gene product. The cancer peptides are also useful as diagnostic agent to detect the presence of cancer, to enhance

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OM protein - protein search, using SW model

Run on: June 22, 2004, 08:49:38 : Search time 11 Seconds

(without alignments)

46.933 Million cell updates/sec

Title: US-09-529-206D-4_COPY_127_136

Perfect score: 47

Sequence: 1 TVGZNLTIR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents At:*

1: /cgna_6/ptodata/2/iaa/5a/COMB.pep:*

2: /cgna_6/ptodata/2/iaa/5b/COMB.pep:*

3: /cgna_6/ptodata/2/iaa/6a/COMB.pep:*

4: /cgna_6/ptodata/2/iaa/6b/COMB.pep:*

5: /cgna_6/ptodata/2/iaa/9ctus/COMB.pep:*

6: /cgna_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	47	100.0	18	US-09-359-503-9
2	47	100.0	18	US-09-359-503-13
3	47	100.0	180	US-08-791-495-9
4	47	100.0	180	US-08-163B-8
5	47	100.0	180	US-09-751-798-8
6	47	100.0	180	US-09-392-114-25
7	42	89.4	9	US-09-344-040C-125
8	42	89.4	9	US-09-833-039A-125
9	38	80.9	9	US-09-344-040C-120
10	38	80.9	9	US-09-833-039A-120
11	38	80.9	180	US-08-911-995-7
12	74.5	342	4	US-09-134-001C-5428
13	72.3	149	4	US-09-540-236-2614
14	34	72.3	177	US-09-132-10-1076
15	33	70.2	97	US-08-118-070-329
16	33	70.2	97	PCT-US93-0528-129
17	33	70.2	109	US-09-341-461-35
18	33	70.2	362	US-09-134-001C-209
19	33	70.2	379	US-08-118-070-32
20	33	70.2	379	PCT-US93-0528-32
21	33	70.2	470	US-09-292-071-25
22	33	70.2	470	US-09-292-071-25
23	33	70.2	470	US-09-767-013-25
24	33	70.2	470	US-09-292-072-25
25	33	70.2	471	US-07-817-020-8
26	33	70.2	471	US-07-996-072A-11
27	33	70.2	471	US-08-370-542-7

ALIGNMENTS

RESULT 1
US-09-359-503-9
Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; TITLE OF INVENTION: Method for Determining Status of A
; Cancers Condition By Determining Antibodies
; to NY
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fabbricht & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,263
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 03-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 625163man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid

RESULT 3
 US-09-359-503-9
 TOPOLOGY: linear
 Query Match 100.0%; Score 47; DB 3; Length 18
 Best Local Similarity 100.0%; Pred. No. 0.008; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TVSGNLTIR 10
 Db 7 TVSGNLTIR 16

RESULT 2
 US-09-359-503-13
 Sequence 13, Application US/09359503
 Patent No. 6251603
 GENERAL INFORMATION:
 APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
 TITLE OF INVENTION: Method for Determining Status of A
 TITLIE OF INVENTION: Cancerous Condition By Determining Antibodies
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/359,503
 FILING DATE: July 23, 1999
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/165,546
 FILING DATE: October 2, 1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/062,422
 FILING DATE: April 17, 1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/937,263
 FILING DATE: September 15, 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/752,182
 FILING DATE: 03-October-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6251603man D.
 REGISTRATION NUMBER: 30,946
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3000
 TELEFAX: (212) 752-5358
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 18 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-359-503-13

Query Match 100.0%; Score 47; DB 3; Length 18;
 Best Local Similarity 100.0%; Pred. No. 0.008; Gaps 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TVSGNLTIR 10
 Db 1 TVSGNLTIR 10

RESULT 4
 US-08-37-263B-8
 Sequence 8, Application US/08937263B
 Patent No. 6274145
 GENERAL INFORMATION:
 APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
 APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
 APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
 TITLE OF INVENTION: ISOLATED NUCLEAR ACID MOLECULE
 TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
 TITLE OF INVENTION: ITSELF, AND USERS THEREOF
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103
 COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/937,263B
 FILING DATE: September 15, 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/725,182
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Sinn, Eric, Patent Agent
 REGISTRATION NUMBER: 40,177
 REFERENCE/DOCKET NUMBER: LUD 5466.1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-1000
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180
 TYPE: amino acid
 TOPOLOGY: linear
 US-08-937-263B-8

Query Match 100.0%; Score 47; DB 3; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Missmatches 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 5
 US-09-751-798-8 Application US/09751798
 / Sequence 8, Application US/09751798
 / GENERAL INFORMATION:
 / APPLICANT: Stockert, Elisabeth; Jager, Elke;
 / APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
 / APPLICANT: Knuth, Alexander; Old, Lloyd J.
 / TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
 / TITLE OF INVENTION: Associated Proteins, Uses Thereof,
 / TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
 / TITLE OF INVENTION: Binding Peptides Derived Therefrom
 / NUMBER OF SEQUENCES: 8
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEES: Fulbright & Jaworski, L.L.P.
 / STREET: 666 Fifth Avenue
 / CITY: New York City
 / STATE: New York
 / COUNTRY: USA
 / ZIP: 10103

PRIOR APPLICATION DATA:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/751,798
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/062,422
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 6523177man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-168

TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-751-798-8

Query Match 100.0%; Score 47; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Missmatches 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 6
 US-09-392-714-25
 / Sequence 25, Application US/09392714A
 / Patent No. 6686147
 / GENERAL INFORMATION:
 / APPLICANT: Scanlan, Matthew J.
 / APPLICANT: Gure, Ali O.
 / APPLICANT: Chen, Yao-Tseng
 / APPLICANT: Old, Lloyd J.
 / TITLE OF INVENTION: Cancer Associated Antigens and Uses
 / FILE REFERENCE: L0461/7062
 / CURRENT APPLICATION NUMBER: US/09/392,714A
 / EARLIER APPLICATION NUMBER: PCT/US98/14679
 / NUMBER OF SEQ ID NO: 30
 / SOFTWARE: FastSEQ for Windows Version 3.0
 / SEQ ID NO: 25
 / LENGTH: 180
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / 09-392-714-25

Query Match 100.0%; Score 47; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.11; Indels 0; Gaps 0;
 Matches 10; Conservative 0; Missmatches 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 7
 US-09-344-040C-125
 / Sequence 125, Application US/09344040C
 / Patent No. 6548064
 / GENERAL INFORMATION:
 / APPLICANT: Turci, Ozlem
 / APPLICANT: Sabin, Ugur
 / APPLICANT: Pfreundschuh, Michael
 / APPLICANT: Ramensee, Hans Georg
 / APPLICANT: Stevanovic, Stefan
 / TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining Expression of an SSX Gene
 / TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene
 / FILE REFERENCE: LUD 5556.1
 / CURRENT APPLICATION NUMBER: US/09/344,040C
 / CURRENT FILING DATE: 1999-06-25
 / PRIOR APPLICATION NUMBER: US 09/105,839
 / PRIOR FILING DATE: 1998-06-26
 / PRIOR APPLICATION NUMBER: US 08/851,130
 / PRIOR FILING DATE: 1997-05-05
 / NUMBER OF SEQ ID NOS: 132
 / SEQ ID NO: 125

FILING DATE: US-09-540-236-2614

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Van Amsterdam, John R.

REGISTRATION NUMBER: 40,212

REFERENCE/DOCKET NUMBER: 10461/7005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-720-3500

TELEFAX: 617-720-2441

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 180 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-791-495-7

Query Match 80.9%; Score 38; DB 2; Length 180;
Best Local Similarity 80.0%; Pred. No. 5.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 127 TVSGNLFIR 136

RESULT 12

US-09-134-001C-5428

Sequence 5428, Application US/09134001C

PATENT NO. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

PRIOR APPLICATION NUMBER: 1998-08-13

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 342

TYPE: PRT

ORGANISM: *Staphylococcus epidermidis*

US-09-134-001C-5428

Query Match 74.5%; Score 35; DB 4; Length 342;
Best Local Similarity 70.0%; Pred. No. 4.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 251 TVGNTIKR 260

RESULT 13

US-09-540-236-2614

Sequence 2614, Application US/09540236

PATENT NO. 6673910

GENERAL INFORMATION:

APPLICANT: Gary L. Bretton et al.

TITLE OF INVENTION: NUCLEARIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS

FILE REFERENCE: 2709 2005-001

CURRENT APPLICATION NUMBER: US/09/540,236

NUMBER OF SEQ ID NOS: 3840

SEQ ID NO. 2614

LENGTH: 149

TYPE: PRT

ORGANISM: *M.catarrhalis*

US-09-540-236-2614

Query Match 72.3%; Score 34; DB 4; Length 149;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 129 TVGNTIKR 138

RESULT 14

US-09-732-210-1076

Sequence 1076, Application US/09732210

PATENT NO. 6573361

GENERAL INFORMATION:

APPLICANT: Bunkers, Greg J.

APPLICANT: Liang, Jihong

APPLICANT: Mittane, Cindy A.

APPLICANT: Seale, Jeffrey W.

APPLICANT: Wu, Yonnie S.

TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use

FILE REFERENCE: 38-21(15036)B

CURRENT APPLICATION NUMBER: US/09/732,210

CURRENT FILING DATE: 2000-12-07

PRIOR APPLICATION NUMBER: US 60/169,513

PRIOR FILING DATE: 1999-12-07

PRIOR APPLICATION NUMBER: US 60/169,340

PRIOR FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 1753

SEQ ID NO. 1076

LENGTH: 177

TYPE: PRT

ORGANISM: *Bacillus stearothermophilus*

US-09-732-210-1076

Query Match 72.3%; Score 34; DB 4; Length 177;
Best Local Similarity 55.6%; Pred. No. 34;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 9
Db 43 TVGNTVRY 51

RESULT 15

US-09-118-270-329

Sequence 329, Application US/08118270

PATENT NO. 5508384

GENERAL INFORMATION:

APPLICANT: Schuster, David I.

TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF

NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWNDY AND NEIMARK

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/08/118,270

FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/118,270

FILING DATE: 09-SEP-1993

PRIOR APPLICATION NUMBER: US 07/943,236

FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3228
TELEX: 248633
INFORMATION FOR SEQ ID NO: 329:
SEQUENCE CHARACTERISTICS:
LENGTH: 97 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-329

Query Match 70.2%; Score 33; DB 1; Length 97;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TVSGNLTI 9
Db 17 TIAGNLYI 25

Search completed: June 22, 2004, 08:54:48
Job time : 11 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:51:28 ; Search time 26 Seconds
Perfect score: 47 ; without alignments

108.582 Million cell updates/sec

Title: US-09-529-206D-4_COPY_127_136

Sequence: 1 TVSGNFTIR 10

Scoring table: BLOSUM62

Gappx 10.0 , Gapext 0.5

Searched: 1163542 seqs, 282313646 residues

Total number of hits satisfying chosen parameters: 1163542

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpat/2/patent/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpat/2/patent/US05_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpat/2/patent/US05_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpat/2/patent/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpat/2/patent/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpat/2/patent/US05_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpat/2/patent/US05_NEW_PUB.pep:*

8: /cgn2_6/ptodata/2/pubpat/2/patent/US08_PUBTOMB.pep:*

9: /cgn2_6/ptodata/2/pubpat/2/patent/US08_PUBCOMB.pep:*

10: /cgn2_6/ptodata/2/pubpat/2/patent/US08_PUBCOMB.pep:*

11: /cgn2_6/ptodata/2/pubpat/2/patent/US09_PUBCOMB.pep:*

12: /cgn2_6/ptodata/2/pubpat/2/patent/US10_PUB.pep:*

13: /cgn2_6/ptodata/2/pubpat/2/patent/US10_PUBCOMB.pep:*

14: /cgn2_6/ptodata/2/pubpat/2/patent/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/2/pubpat/2/patent/US10_PUBCOMB.pep:*

16: /cgn2_6/ptodata/2/pubpat/2/patent/US10_NEW_PUB.pep:*

17: /cgn2_6/ptodata/2/pubpat/2/patent/US10_PUBCOMB.pep:*

18: /cgn2_6/ptodata/2/pubpat/2/patent/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	20	15 US-10-164_121A-35	Sequence 35 , App1
2	47	100.0	20	15 US-10-164_07BA-34	Sequence 34 , App1
3	47	100.0	30	12 US-10-296_734-1414	Sequence 1414 , App1
4	47	100.0	54	16 US-10-447_161-140	Sequence 140 , App1
5	47	100.0	180	9 US-09-751-798-8	Sequence 8 , App1
6	47	100.0	180	10 US-09-849_602-30	Sequence 30 , App1
7	47	100.0	180	12 US-10-296_734-832	Sequence 82 , App1
8	47	100.0	180	13 US-10-023-182-8	Sequence 8 , App1
9	47	100.0	180	14 US-10-207_655-1	Sequence 71 , App1
10	47	100.0	180	15 US-10-026_066-3	Sequence 3 , App1
11	47	100.0	180	15 US-10-117_937-74	Sequence 74 , App1
12	47	100.0	180	15 US-10-295_027-186	Sequence 386 , App1
13	47	100.0	180	16 US-10-188_832-139	Sequence 139 , App1
14	47	100.0	397	9 US-09-821-883-27	Sequence 27 , App1
15	47	100.0	3541	12 US-10-296_734-1454	Sequence 1454 , App1

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	42	89.4	9	14 US-09-833-039-1225	Sequence 125 , App
2	42	89.4	9	14 US-10-177-277-125	Sequence 125 , App
3	42	89.4	9	15 US-10-117-937-185	Sequence 185 , App
4	38	80.9	10	15 US-10-117-937-186	Sequence 186 , App
5	38	80.9	9	10 US-09-923-039-120	Sequence 120 , App
6	38	80.9	9	14 US-10-177-277-120	Sequence 120 , App
7	38	80.9	10	12 US-10-296_734-1446	Sequence 1446 , App
8	38	80.9	12	US-10-296_734-834	Sequence 834 , App
9	38	80.9	14	US-10-116-473-69	Sequence 69 , App1
10	38	80.9	14	US-10-117-937-75	Sequence 75 , App1
11	38	80.9	12	US-10-282-1224-71904	Sequence 61146 , A
12	38	78.7	130	12 US-10-092-900A-196	Sequence 196 , App
13	35	74.5	317	12 US-10-092-900A-196	Sequence 7104 , A
14	35	74.5	335	9 US-09-815-242-12730	Sequence 12230 , A
15	35	74.5	335	12 US-10-282-1224-70259	Sequence 70259 , A
16	35	74.5	335	12 US-10-282-1224-70661	Sequence 70661 , A
17	35	74.5	336	13 US-10-106-605-203	Sequence 203 , App
18	35	74.5	349	12 US-10-424-599-174030	Sequence 174030 , App
19	35	74.5	349	15 US-10-074-978A-399	Sequence 399 , App
20	35	74.5	349	15 US-10-013-379-6	Sequence 6 , App1
21	35	74.5	349	14 US-10-060-793B-6	Sequence 6 , App1
22	35	74.5	349	12 US-10-219-535-242	Sequence 242 , App
23	35	74.5	349	12 US-10-232-224-242	Sequence 242 , App
24	34	72.3	38	12 US-10-222-884-242	Sequence 242 , App
25	34	72.3	38	12 US-10-220-163-242	Sequence 242 , App
26	34	72.3	38	12 US-10-218-631-242	Sequence 242 , App
27	34	72.3	38	14 US-10-210-338-242	Sequence 242 , App
28	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
29	34	72.3	38	14 US-10-210-338-242	Sequence 242 , App
30	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
31	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
32	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
33	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
34	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
35	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
36	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
37	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
38	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
39	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
40	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
41	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
42	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
43	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
44	34	72.3	38	14 US-10-218-631-242	Sequence 242 , App
45	34	72.3	38	14 US-10-216-159A-242	Sequence 242 , App

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
2	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
3	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
4	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
5	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
6	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
7	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
8	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
9	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
10	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
11	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
12	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
13	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
14	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
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Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
2	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
3	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
4	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
5	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
6	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
7	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
8	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
9	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
10	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
11	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
12	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
13	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
14	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
15	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;

Result No.	Score	Query Match	Length	DB ID	Description
1	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
2	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
3	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
4	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
5	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
6	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
7	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
8	100.0	15	100.0	100.0	Best Local Similarity 100.0%; Pred. No. 0.0333; Mismatches 0; Indels 0; Gaps 0;
9	100				

APPLICANT: Van der Bruggen, Pierre
 APPLICANT: Boon, Thierry
 TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules and Uses Thereof
 CURRENT APPLICATION NUMBER: US-10/164,078A
 CURRENT FILING DATE: 2002-06-05
 NUMBER OF SEQ ID NOS: 35
 SEQ ID NO: 34
 LENGTH: 20
 TYPE: PRT
 ORGANISM: *H. sapiens*
 FEATURE: US-10-164-078A-34

Query Match 100.0% Score 47; DB 15; Length 20;
 Best Local Similarity 100.0% Prod. No. 0.033; Pred. No. 0.033; Score 47; DB 16; Length 54;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 9 TVSGNLTIR 18

RESULT 3
 Sequence 1414 Application US/10296734
 Publication No. US2004005137A1
 GENERAL INFORMATION:
 APPLICANT: Thompson, Scott A
 APPLICANT: Banshaw, Ian A
 TITLE OF INVENTION: Synthetic molecules and uses therefor
 CURRENT APPLICATION NUMBER: US-10/296,734
 CURRENT FILING DATE: 2003-08-04
 PRIOR APPLICATION NUMBER: AU-007761/00
 PRIOR FILING DATE: 2000-05-26
 NUMBER OF SEQ ID NOS: 1567
 SEQ ID NO: 1414
 LENGTH: 20
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: NYSora segment 9
 US-10-296-734-1414

Query Match 100.0% Score 47; DB 12; Length 30;
 Best Local Similarity 100.0% Prod. No. 0.051; Pred. No. 0.051; Score 47; DB 16; Length 54;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 9 TVSGNLTIR 18

RESULT 4
 Sequence 140 Application US/10447161
 Publication No. US2004002331A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Rong-fu
 TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
 FILE REFERENCE: HO-00248AUS1
 CURRENT FILING DATE: 2003-05-28
 PRIOR APPLICATION NUMBER: 60/183,530
 PRIOR FILING DATE: 2000-05-28
 NUMBER OF SEQ ID NOS: 148
 SEQ ID NO: 140
 LENGTH: 54
 TYPE: PRT
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: Synthetic Peptide
 US-10-447-161-140

Query Match 100.0% Score 47; DB 16; Length 54;
 Best Local Similarity 100.0% Prod. No. 0.097; Pred. No. 0.097; Score 47; DB 16; Length 54;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 25 TVSGNLTIR 34

RESULT 5
 Sequence 8 Application US/09751798
 Publication No. US20010321A1
 GENERAL INFORMATION:
 APPLICANT: Stockert, Elisabeth; Jager, Elke;
 APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
 APPLICANT: Knuth, Lloyd J.
 APPLICANT: Antibodies Which Bind to NY-ESO-1, Cancer Associated Proteins Uses Thereof, Truncated Forms of NY-ESO-1, and HLA Binding Peptides Derived Therefrom
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEES: Bulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103
 COMPUTER READABLE FORM:
 COMPUTER: IBM
 MEDIUM TYPE: Diskette
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 COMPUTER: IBM
 APPLICATION NUMBER: US/09/751,798
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/062,422
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/062,422
 FILING DATE:
 APPLICATION NUMBER: 09/725,182
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. US2002010321Alman D.
 REGISTRATION NUMBER: 30,945
 REFERENCE/DOCKET NUMBER: LUD 5466.3
 TELECOMMUNICATION:
 TELEPHONE: (212) 318-3168
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180
 TYPE: amino acid
 TOPOLOGY: linear
 US-09-751-798-8

Query Match 100.0% Score 47; DB 9; Length 180;
 Best Local Similarity 100.0% Prod. No. 0.36; Pred. No. 0.36; Score 47; DB 9; Length 180;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 6
 Sequence 30 Application US/09849602
 Publication No. US-09-849-602-30
 Sequence 30

Publication No. US20030165834A1
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Matthew J.
 APPLICANT: Old, Lloyd J.
 APPLICANT: Stochert, Elisabeth
 APPLICANT: Chen, Yao-Tseng
 TITLE OF INVENTION: Colon Cancer Antigen Panel
 FILE REFERENCE: L04617105 (JRV)
 CURRENT APPLICATION NUMBER: US09/849,602
 CURRENT FILING DATE: 2001-05-04
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 30
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-849-602-30

Query Match 100.0%; Score 47; DB 10; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 7
 US-10-296-734-832
 ; Sequence 832, Application US/10296734
 ; Publication No. US20040045413A1
 GENERAL INFORMATION:
 APPLICANT: Thompson, Scott A
 APPLICANT: Ramshaw, Ian A
 TITLE OF INVENTION: Synthetic molecules and uses therefor
 FILE REFERENCE: Savine
 CURRENT APPLICATION NUMBER: US10/296,734
 CURRENT FILING DATE: 2003-08-04
 PRIOR APPLICATION NUMBER: AU PCT7761/00
 PRIOR FILING DATE: 2000-05-26
 NUMBER OF SEQ ID NOS: 1507
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 832
 LENGTH: 180
 TYPE: PRT
 OTHER INFORMATION: NYNS01a consensus polypeptide

Query Match 100.0%; Score 47; DB 12; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 8
 US-10-023-182-8
 ; Sequence 8, Application US/10023182
 ; Publication No. US20020164655A1
 GENERAL INFORMATION:
 APPLICANT: Stockert, Elisabeth; Jager, Bile;
 APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
 APPLICANT: Knuth, Alexander; Old, Lloyd J.
 TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
 Associated Proteins, Uses Thereof, Truncated Forms of NY-ESO-1, and HLA
 Truncated Peptides Derived Therefrom
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:

ADDRESS: Fulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/023,182
 FILING DATE: 17-Dec-2001
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/751,798
 FILING DATE: December 29, 2000
 APPLICATION NUMBER: 09/062,122
 FILING DATE: <Unknown>
 APPLICATION NUMBER: 08/725,182
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. US20020164665A1man, D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LJD 5466-3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3168
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180
 TYPE: amino acid
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-10-023-182-8

Query Match 100.0%; Score 47; DB 13; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 9
 US-10-207-655-71
 ; Sequence 71, Application US/10207655
 ; GENERAL INFORMATION:
 ; Publication No. US20030118592A1
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Hayden-Ledbetter, Martha S.
 ; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
 ; FILE REFERENCE: 390069.401C1
 ; CURRENT APPLICATION NUMBER: US/10/207,655
 ; NUMBER OF SEQ ID NOS: 426
 ; SOFTWARE: Patentin version 3.0
 ; SEQ ID NO: 71
 ; LENGTH: 180
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-207-655-71

Query Match 100.0%; Score 47; DB 14; Length 180;
 Best Local Similarity 100.0%; Pred. No. 0.36;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 8
 US-10-023-182-8
 ; Sequence 8, Application US/10023182
 ; Publication No. US20020164655A1
 GENERAL INFORMATION:
 APPLICANT: Stockert, Elisabeth; Jager, Bile;
 APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
 APPLICANT: Knuth, Alexander; Old, Lloyd J.
 TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
 Associated Proteins, Uses Thereof, Truncated Forms of NY-ESO-1, and HLA
 Truncated Peptides Derived Therefrom
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:

RESULT 10
 US-10-026-066-3
 Sequence 3, Application US/10026066
 Publication No. US20030215425A1
 GENERAL INFORMATION:
 APPLICANT: Simard, John J. E.
 TITLE OF INVENTION: EPITOPE SYNCHRONIZATION IN ANTIGEN
 FILE REFERENCE: CTLIIM 21CPLIC
 CURRENT APPLICATION NUMBER: US/10/026, 066
 CURRENT FILING DATE: 2001-12-07
 PRIOR APPLICATION NUMBER: 09/561, 074
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 09/560, 465
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 09/561, 572
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 09/561, 571
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: PCT/US01/13806
 PRIOR FILING DATE: 2001-04-27
 NUMBER OF SEQ ID NOS: 89
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-026-066-3

Query Match 100.0% Score 47; DB 15; Length 180;
 Best Local Similarity 100.0% Pred. No. 0.36%;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO 3

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 11
 US-10-117-937-74
 Sequence 74, Application US/10117937
 Publication No. US2003022039A1
 GENERAL INFORMATION:
 APPLICANT: CTL IMMUNO THERAPIES CORP.
 SIMARD, John, J.L.
 APPLICANT: DIAMOND, David, C.
 APPLICANT: LIU, Liping
 APPLICANT: XIE, Zhidong
 TITLE OF INVENTION: EPITOPE SEQUENCES
 FILE REFERENCE: CTLIIM, 027A
 CURRENT APPLICATION NUMBER: US/10/117, 937
 CURRENT FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: US 60/282, 211
 PRIOR FILING DATE: 2001-04-06
 PRIOR APPLICATION NUMBER: US 60/337, 017
 PRIOR FILING DATE: 2001-11-07
 PRIOR APPLICATION NUMBER: US 60/363, 210
 PRIOR FILING DATE: 2002-03-07
 NUMBER OF SEQ ID NOS: 602
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 74
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-117-937-74

Query Match 100.0% Score 47; DB 15; Length 180;
 Best Local Similarity 100.0% Pred. No. 0.36%;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SEQ ID NO 74

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 12
 US-10-95-027-386
 Sequence 386, Application US/10295027
 Publication No. US20030232350A1
 GENERAL INFORMATION:
 APPLICANT: Afar, Daniel
 AZIZ, Natasha
 GINSBERG, Wendy M.
 APPLICANT: Gish, Kurt C.
 APPLICANT: Glynn, Richard
 APPLICANT: Heverzi, Peter A.
 APPLICANT: Mack, David H.
 APPLICANT: Murray, Richard
 APPLICANT: Watson, Susan R.
 APPLICANT: BOS BIOTECHNOLOGY, INC.
 TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
 Methods of Screening for Modulators of Cancer
 FILE REFERENCE: 018501-012500US
 CURRENT APPLICATION NUMBER: US/10/295, 027
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663, 733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350, 665
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/335, 394
 PRIOR FILING DATE: 2001-11-15
 PRIOR APPLICATION NUMBER: US 60/332, 464
 PRIOR FILING DATE: 2001-11-21
 PRIOR APPLICATION NUMBER: US 60/334, 393
 PRIOR FILING DATE: 2001-11-29
 PRIOR APPLICATION NUMBER: US 60/340, 376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347, 211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347, 349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355, 250
 PRIOR FILING DATE: 2002-02-08
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 1386
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 386
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens

US-10-295-027-386

Query Match 100.0% Score 47; DB 15; Length 180;
 Best Local Similarity 100.0% Pred. No. 0.36%;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

RESULT 13
 US-10-188-832-139
 Sequence 139, Application US/10188832
 Publication No. US20040076955A1
 GENERAL INFORMATION:
 APPLICANT: AZIZ, Natasha
 APPLICANT: BOS BIOTECHNOLOGY, INC.
 TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
 and Methods of Screening for Modulators of Bladder
 TITLE OF INVENTION: Cancer
 FILE REFERENCE: 018501-002330US

Qy 1 TVSGNLTIR 10
 Db 127 TVSGNLTIR 136

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; CURRENT APPLICATION NUMBER: US/10/188, 832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,999
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-139

Query Match 100.0%; Score 47; DB 16; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.36;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 127 TVSGNLTIR 136

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RESULT 14
US-09-821-883-27
; Sequence 27, Application US/09821883
; Patent No. US200611310A1
; GENERAL INFORMATION:
; APPLICANT: Laus, Reiner
; APPLICANT: Vidovic, Damir
; APPLICANT: Graddis, Thomas
; TITLE OF INVENTION: Compositions and Methods for Dendritic
; FILE REFERENCE: 7636-0022-10
; CURRENT APPLICATION NUMBER: US/09/821,883
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 60/193,504
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows version 4.0
; SEQ ID NO 27
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: NY-ESO-1C tumor antigen
US-09-821-883-27

Query Match 100.0%; Score 47; DB 9; Length 397;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 127 TVSGNLTIR 136

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RESULT 15
US-10-296-734-1454
; Sequence 1454, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A.
; APPLICANT: Ramsaw, Ian A.
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:48:03 ; Search time 9 Seconds

106,879 Million cell updates/sec

Title: US-09-529-2004D-4_COPY_127_136

Perfect score: 47

Sequence: 1 TVSGNLTIFR 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 0000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:
 1: p1r1:
 2: p1r2:
 3: p1r3:
 4: p1r4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	76.6	245	2 T13099	major tail protein
2	36	76.6	323	2 AD2753	lipoic Acid Synthe
3	36	76.6	323	2 B97534	lipoic acid synthe
4	34	74.5	335	2 A98937	hypothetical prote
5	34	72.3	177	1 P5BSOF	ribosomal protein
6	34	72.3	244	2 T41234	translation initia
7	34	72.3	311	2 AB3218	2-hydroxyacid dehy
8	34	72.3	314	2 Q86835	hypothetical prote
9	34	72.3	1266	2 A85989	hypothetical prote
10	34	72.3	1266	2 AB1143	tail fiber protein
11	33	70.2	144	1 TPBPPI	gene R protein - B
12	33	70.2	144	2 S18683	MAT2 efflux family
13	33	70.2	411	2 A11241	hypothetical prote
14	33	70.2	426	2 B98106	hypothetical prote
15	33	70.2	428	2 P85253	probable amino-acid
16	33	70.2	436	2 AB1977	N-acetylglutamate
17	33	70.2	436	2 AB1033	serotonin receptor
18	33	70.2	449	2 S02011	serotonin receptor
19	33	70.2	471	2 A34863	5-hydroxytryptamin
20	33	70.2	471	2 S40689	serotonin receptor
21	33	70.2	471	2 S11280	serotonin receptor
22	33	70.2	471	2 A43956	hypothetical prote
23	33	70.2	876	2 E96674	probable TMV resis
24	33	70.2	918	2 T02759	hypothetical prote
25	32	1996	2 F71405	probable integral	
26	32	68.1	102	2 C86898	conserved hypothet
27	32	68.1	121	2 AB1972	5-HT2 receptor -
28	32	68.1	135	2 DB1029	
29	32	68.1	187	2 I37105	

ALIGNMENTS

RESULT 1

T13099
 major tail protein V - phage N15

N;Alternate name: Protein qpl3

C;Species: Phage N15

C;Date: 13-Aug-1999 #Sequence_revision 13-Aug-1999 #text_change 13-Aug-1999

C;Accession: T13099

R;Hendrix, R.W.; Ravin, V.K.; Casjens, S.R.; Ford, M.B.; Smirnov, I.K.; submitted to the EMBL Data Library, May 1998

A;Reference number: 217603

A;Accession: T13099

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Residues: 1-245 <HENV>

A;Cross references: EMBL:AF064539; NID:93192683; PID:93192697; PID: AAC19050.1

A;Note: Gene 13

C;Genetics:

C;Superfamily: phage lambda major tail protein V

Query Match Similarity 76.6%; Score 36; DB 2; Length 245;

Best Local Similarity 77.8%; Prod. No. 13;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 TVSGNLT 9
 ||||| | | | |;
 Db 209 TVSGNLT 217

RESULT 2

AD2753 Lipoc Acid Synthetase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)

C;Species: Agrobacterium tumefaciens

C;Accession: AD2753

C;Accession: AD2753

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Ergec, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, F.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S.; Science 294, 2317-2323, 2001

A;Authors: Woo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, B.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:1143193

A;Accession: AD2753

A;Molecule type: DNA

A;Genetics:

A;Cross references: GB:AE008688; PID:AA142442.1; PMID:21608550; Dupont

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Map position: circular chromosome

A;Map position: lipoic acid synthase

C;Superfamily: lipoic acid synthase

ribosomal protein L6 - *Bacillus stearothermophilus*
 N; Alternate name: ribosomal protein BL10
 C; Species: *Bacillus stearothermophilus*
 C; Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 12-Jun-2003
 C; Accession: A02766; B39085; S59061
 R; Kimura, M.; Rawlings, N.; Apelt, K.
 FEBS Lett. 136, 58-61, 1981
 A; Title: The amino acid sequence of protein BL10 from the 50S subunit of the *Bacillus* s-
 A; Reference number: A02766
 A; Accession: A02766
 A; Molecule type: protein
 A; Residues: 1-177 <KIM>
 R; Ramakrishnan, V.; Gerchman, S.E.
 J. Biol. Chem. 266, 880-885, 1991
 A; Title: Cloning, sequencing, and overexpression of genes for ribosomal proteins from *B*
 C; Accession: B97534
 A; Reference number: A39085; MUID:91093267; PMID:1985969
 A; Accession: B39085
 A; Molecule type: protein
 A; Residues: 8-170 <DAW>
 A; Cross-references: GB:MS75622
 R; Urlaub, H.; Kraft, V.; Bischoff, O.; Mueller, E.C.; Wittmann-Liebold, B.
 EMBO J. 14, 4578-4588, 1995
 A; Title: Protein-rRNA binding features and their structural and functional implications
 C; Accession: S59051
 A; Reference number: S59051; MUID:96003638; PMID:7556101
 A; Accession: S59061
 A; Molecule type: protein
 A; Residues: 149-163 <URL>
 C; Superfamily: ribosomal protein L6/L9
 C; Keywords: protein biosynthesis; ribosome
 C; Superfamily: circular chromosome
 C; Superfamily: lipopid acid synthase

Query Match 76.6% Score 36; DB 2; Length 323;
 Best Local Similarity 70.0%; Pred. No. 18; Indels 2; Gaps 0;
 Matches 7; Conservative 1; Mismatches 2;
 Qy 1 TVSGNLTIR 10
 Db 189 TVGENYLTVR 198

RESULT 3

B97534
 Biotin acid synthetase (lip-syn) (lipope synthase) [imported] - *Agrobacterium tumefaciens*
 C; Species: *Agrobacterium tumefaciens*
 C; Accession: B97534
 C; Sequence: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
 R; Godner, B.; Hinkle, G.; Gactung, S.; Miller, N.; Quroollo, B.; Goldman, M.; Liu, F.; Wollam, A.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
 A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
 A; Accession: B97534
 A; Reference number: A97359; MUID:21608551; PMID:11743194
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-323 <KUR>
 A; Cross-references: GB:AE007869; PIDN:AAK81227.1; PID:gi15156511; GSPDB:GN00169
 C; Genetics:
 A; Gene: AGR C 2646
 A; MAF position: circular chromosome
 C; Superfamily: lipopid acid synthase

Query Match 76.6% Score 36; DB 2; Length 323;
 Best Local Similarity 70.0%; Pred. No. 18; Indels 2; Gaps 0;
 Matches 7; Conservative 1; Mismatches 2;
 Qy 1 TVSGNLTIR 10
 Db 189 TVGENYLTVR 198

RESULT 4

A89837
 hypothetical protein Ska0619 [imported] - *Staphylococcus aureus* (strain N315)
 C; Species: *Staphylococcus aureus* (strain N315)
 C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 01-Mar-2002
 C; Accession: A89837
 R; Kurada, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uji, Y.; Hattori, M.; Sawayano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiota, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lacet, 357, 1225-1240, 2001
 A; Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
 A; Accession number: A89758; MUID:21311952; PMID:11418146
 A; Status: preliminary
 A; Molecule type: DNA
 A; Residues: 1-335 <KUR>
 A; Cross-references: GB:BA000018; PIDN:913700555; PIDN:BA841852.1; GSPDB:GN00149
 C; Experimental source: strain N315
 A; Gene: SA0619
 C; Superfamily: probable sodium-dependent phosphate transporter MTH1885
 Query Match 74.5% Score 35; DB 2; Length 335;
 Best Local Similarity 70.0%; Pred. No. 29; Indels 2; Gaps 0;
 Matches 7; Conservative 1; Mismatches 2;
 Qy 1 TVSGNLTIR 10
 Db 245 TVGENIMKIR 254

RESULT 5

R55S0F

Query Match 72.3% Score 34; DB 2; Length 244;
 Best Local Similarity 75.0%; Pred. No. 33; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Mismatches 1;
 C; Superfamily: conserved hypothetical protein YPR016C
 Query Match 72.3% Score 34; DB 2; Length 244;
 Best Local Similarity 75.0%; Pred. No. 33; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Mismatches 1;
 Qy 1 TVSGNLTIR 8
 Db 141 TVAGNIVTV 148

RESULT 6

T41234
 translation initiation factor eIF-6 [imported] - fission yeast (Schizosaccharomyces pombe)
 C; Species: *Schizosaccharomyces pombe*
 C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 15-Sep-2000
 C; Accession: T41234
 R; Lyne, M.; Harris, D.E.; Murphrey, L.D.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Database Library, January 1999
 A; Reference number: Z21979
 A; Accession: T41234
 A; Status: preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-244 <DN>
 A; Cross-references: EMBL:AL035075; PIDN:CAA22640.1; GSPDB:GN000668; SPDB:SPCC1919.09
 A; Experimental source: strain 972h-; cosmid c1919
 C; Genetics:
 A; Gene: SPDB:SPCC1919.09
 A; Map Position: 3
 A; Introns: 12/2; 36/2
 C; Superfamily: conserved hypothetical protein YPR016C
 Query Match 72.3% Score 34; DB 2; Length 244;
 Best Local Similarity 75.0%; Pred. No. 33; Indels 0; Gaps 0;
 Matches 6; Conservative 2; Mismatches 1;
 Qy 1 TVSGNLTIR 8
 Db 141 TVAGNIVTV 148

RESULT 7

AB3218
 2-hydroxyacid dehydrogenase Atu5474 [imported] - *Agrobacterium tumefaciens* (strain C58,
 C; Species: *Agrobacterium tumefaciens*

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C;Accession: AB3218
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 an, P.; Roncero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jurg, M.; Kespas, W.; Perry, M.; Gordon-Kamm,
 M.; Ster, E.W.
 A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A;Reference number: AB2277; MUID:21608550; PMID:11743193
 A;Accession: AB3218
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-311 <KUR>
 A;Cross-references: GB:AE008687; PIDN:AAL4160.1; PMID:917743930; GSPDB:GN00188
 A;Experimental source: strain C58 (Dupont)
 C;Genetics:
 A;Gene: Atu5474
 A;Molecule: plasmid
 C;Superfamily: phosphoglycerate dehydrogenase
 Query Match 72.3%; Score 34; DB 2; Length 311;
 Best Local Similarity 77.8%; Pred. No. 43;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 VSGNLTIR 10
 Db 288 VAGNLTYR 296

RESULT 8
 A;hypothetical protein YreB [imported] - Lactococcus lactis subsp. lactis (strain III403)
 C;Species: Lactococcus lactis subsp. lactis
 C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
 R;Boilot, A.; Wincker, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissbach, J.; Ehrli
 Genome Res. 11, 731-753, 2001
 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
 A;Reference number: AB66325; MUID:21235186; PMID:1133771
 A;Accession: AB66325
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-314 <STO>
 A;Cross-references: GB:AE005176; PIDN:912724702; PIDN:AAK05785.1; GSPDB:GN00146
 A;Experimental source: strain III403
 C;Genetics:
 A;Gene: yreB

Query Match 72.3%; Score 34; DB 2; Length 314;
 Best Local Similarity 75.0%; Pred. No. 44;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 VSGNLTIR 9
 Db 93 ISGNLTIR 100

RESULT 9
 A85983
 hypothetical protein Z4694, [imported] - Escherichia coli (strain O157:H7, substrain EDL9
 C;Species: Escherichia coli
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glassner, J.D.; Rose, D.J.; Mayhew
 iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A;Reference number: A85480; MUID:21074935; PMID:11206551
 A;Accession: A85983
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1266 <STO>

A;Cross-references: GB:AE005174; NID:91217869; PIDN:AA58373.1; GSPDB:GN00145; UWGP:24
 A;Experimental source: strain O157:H7, substrain EDL933
 C;Genetics:
 A;Gene: Z4604
 C;Superfamily: Escherichia coli hypothetical protein yhdp
 Query Match 72.3%; Score 34; DB 2; Length 1266;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 TVSGNLTIR 9
 Db 1017 TISGNTLTL 1025

RESULT 10
 F91143
 hypothetical protein ECs4118 [imported] - Escherichia coli (strain O157:H7, substrain R:
 C;Species: Escherichia coli
 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 17-May-2002
 R;Accession: F91143
 R;Miyoshi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokota, K.; Han, C.G.
 Gasawara, M.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001
 A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
 A;Reference number: A99629; MUID:21156231; PMID:11258796
 A;Accession: F91143
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1266 <SHAY>
 A;Cross-references: GB:BA0000007; PIDN:BA037541.1; PMID:913363591; GSPDB:GN00154
 A;Experimental source: strain O157:H7, substrain RIMD 0509952
 C;Genetics:
 A;Gene: ECs4118
 C;Superfamily: Escherichia coli hypothetical protein yhdp
 Query Match 72.3%; Score 34; DB 2; Length 1266;
 Best Local Similarity 66.7%; Pred. No. 1.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 TVSGNLTIR 9
 Db 1017 TISGNTLTL 1025

RESULT 11
 TP2PPI
 C;Species: Phage PI
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 23-Jul-1999
 C;Accession: JS0460
 R;Guidolin, A.; Zingg, J.M.; Abre, W.
 Gene 76, 239-243, 1989
 A;Title: Organization of the bacteriophage PI tail-fibre operon.
 A;Reference number: PS0109; MUID:89326122; PMID:2526777
 A;Accession: JS0460
 A;Molecule type: DNA
 A;Residues: 1-144 <GUT>
 A;Cross-references: GB:M25470; NID:9341349; PIDN:AA58777.1; PMID:9538421
 C;Genetics:
 A;Gene: R
 C;Superfamily: phage PI tail fiber protein R
 C;Keywords: tail fiber

RESULT 12

S16683 gene R protein - Escherichia coli plasmid p15B

C;Species: Escherichia coli

C;Accession: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 20-Sep-1999

R;Sandmeier, H.; Iida, S.; Huebner, P.; Hiestand-Nauer, R.; Arber, W.

Nucleic Acids Res. 19, 5831-5839, 1991

A;Reference number: S16680; MUID:92051368; PMID:1945872

A;Accession: S16683

A;Status: translation not shown

A;Molecule type: DNA

A;Residues: 1-144 <SAN>

C;Cross-references: ENBLL:X62121; NID:542224; PIDN:CA44046.1; PMID:942228

C;Genetics:

A;Gene: R

A;Genome: Plasmid

C;Superfamily: Phage PI tail fiber protein R

Query Match 70.2%; Score 33; DB 2; Length 144;

Best Local Similarity 60.0%; Pred. No. 30;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10

Db 79 TVSGNLTIR 98

Qy 1 TVSGNLTIR 10

Db 79 TVSGNLTIR 98

RESULT 13

F85253 hypothetical protein AT4922170 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001

C;Accession: F85253

C;Paronymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spr

Nature 402, 769-771, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.

A;Reference number: A85001; PMID:20083488; PMID:10617198

A;Accession: F85253

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-428 <STO>

C;Genetics:

A;Gene: AT4922170

A;Map Position: 4

C;Superfamily: Arabidopsis thaliana hypothetical protein T12H17.50

C;Accession: G95241

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

R;Tettelein, H.; Nelson, K.B.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid

son, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,

Nelson, T.; Hickney, E.K.; Holt, I.B.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: G95241

A;Status: preliminary

A;Molecule type: DNA

A;Cross-references: GB:AE005672; PIDN:AAK76128.1; PMID:91497357; GSPDB:GN00164; TIGR:SP4

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP2065

RESULT 14

B38106 hypothetical protein MATE transporter [imported] - Streptococcus pneumoniae (strain R6)

C;Species: Streptococcus pneumoniae

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 22-Oct-2001

R;Boskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgert, S.; Dehoff, B.S.; E

Y., P.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; N

J.; Bacteriol. 183, 5709-5717, 2001

A;Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;

A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.

A;Reference number: A97872; MUID:21429245; PMID:11544234

FT	DOMAIN	5	82	GLY-RICH.
FT	TRANSMEM	156	172	POTENTIAL.
SQ	SEQUENCE	180 AA;	17992 MW;	BL22C5C2B1569 CRC64;
Query	Match	100.0%	Score 47;	DB 1; Length 180;
Best Local Similarity	100.0%	Pred. No. 0.024;		
Matches	10;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0
Qy	1	TVSGNLTIR 10		
Db	127	TVSGNLTIR 136		
RESULT 2				
LIPAPHELIET				
ID	LIPA_RHET	STANDARD;	PRT;	322 AA.
AC	005941;			
DT	15-JUL-1998	(Rel. 36, Created)		
DT	15-JUL-1998	(Rel. 36, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Lipoic acid synthetase (Lip-syn)	(Lipoate synthase)		
GN	LIPA.			
OS	Rhizobium etli.			
OC	Bacteria; Protobacteria; Alphaproteobacteria; Rhizobiales;			
OC	Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium;			
OX	NCBI_TaxID:294497;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CEB;			
RX	PubMed=97286510;			
TA	Patraca E.J.; Patraca B.J.; Riccerino M.; Riccerino A.; Taccerino M.			
PA	"Cloning and transcriptional analysis of the lipoa acid synthetase gene from Rhizobium etli."			
RT	FEBS Microbiol. Lett. 149:165-172 (1997).			
RL	-1- FUNCTION: Synthesis of alpha-(-)-lipoic acid. It may be involved in the sulfur insertion chemistry in lipoate biosynthesis (By similarity).			
CC	-1- PATHWAY: Lipoate biosynthesis.			
CC	-1- SUBCELLULAR LOCATION: Cytosolic (By similarity).			
CC	-1- SIMILARITY: Belongs to the biotin and lipoic acid synthetases family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).			
CC				
CC	EMBL: Y11708; CAA72100.1; -.			
DR	HAMAP; MF_00206; -;			
DR	IPRC06638; B1P3.			
DR	InterPro; IPR003698; Lipoate synth.			
DR	InterPro; IPR007197; Radical SAM.			
DR	PF04155; Radical SAM; I.			
DR	SMART; SM00729; B1P3; I.			
DR	TIGRFAMS; TIGR00510; LipA; I.			
KW	Iron-sulfur.			
FT	IRON-SULFUR	(POTENTIAL).		
FT	METAL	87		
FT	METAL	91		
FT	METAL	94		
SQ	SEQUENCE	322 AA;	36297 MW;	45E185215486847 CRC64;
Query	Match	80.9%	Score 38;	DB 1; Length 322;
Best Local Similarity	70.0%	Pred. No. 3.1;		
Matches	7;	Conservative	2; Mismatches 1;	Indels 0; Gaps 0
Qy	1	TVSGNLTIR 10		
Db	188	TVAGNTIVR 197		

FT STRAND 8 9
 FT TURN 12 13
 FT STRAND 15 19
 FT TURN 20 21
 FT STRAND 22 27
 FT TURN 28 29
 FT STRAND 30 35
 FT TURN 38 39
 FT STRAND 41 45
 FT TURN 46 47
 FT STRAND 48 52
 FT HELIX 58 79
 FT TURN 80 80
 FT STRAND 82 89
 FT TURN 91 92
 FT STRAND 94 98
 FT TURN 99 100
 FT STRAND 101 105
 FT STRAND 112 114
 FT TURN 118 119
 FT STRAND 120 126
 FT TURN 127 128
 FT STRAND 129 134
 FT HELIX 137 148
 FT TURN 149 150
 FT STRAND 155 157
 FT TURN 160 163
 FT STRAND 164 165
 SQ SEQUENCE 177 AA; 19168 MW; B4EC662A419616B3 CRC64;

Query Match 72.3%; Score 34; DB 1; Length 177;
 Best Local Similarity 55.6%; Pred. No. 11; Gaps 0;
 Matches 5; Conservative 3; Mismatches 1; Indels 0;
 QY 1 TVSGNLT 9
 DB 43 TVSGNVTY 51

RESULT 6
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 AC 094476; DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2003 (Rel. 42, Last sequence update)
 DE "Bukaryotic translation initiation factor 6 (eIF-6)."
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Bacteria; Fungi; Ascomycota; Schizosaccharomyces;
 OC Schizosaccharomyces; Schizosaccharomyctaceae;
 OC Schizosaccharomyces.
 OX NCBI_TAXID=4896;
 RP SEQUENCE FROM N.A.
 RC STRAIN=72;
 RX MEDLINE=218489401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne R., Stewart A.,
 RA Sacours J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Frazer A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jageels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neil S., Pearson D., Quail M.A., Rabinowitz B.,
 RA Sutherland K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squires R., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Mert R., Robben J., Grymonpre B.,
 RA Weltjens I., Vansstreets E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer S., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Goux S., Lelaike V., Mortier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gallard C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Ruenelt J.L., Moreno S., Armstrong J.L., Forburg S.L.,
 RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potaashkin J.,
 RA Shpalovskii G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of *Schizosaccharomyces pombe*."
 RL Nature 415:871-880(2002).
 CC !- FUNCTION: Binds to the 60S ribosomal subunit and prevents its
 CC association with the 40S ribosomal subunit to form the 80S
 CC initiation complex (By similarity).
 CC !- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
 CC !- SIMILARITY: Belongs to the eIF-6 family.
 CC
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 CC
 EMBL; AL05075; CA22640_1; -.
 DR PIR; T41234; T41234.
 DR HSSP; Q12522; 1G62.
 DR GeneDB; SPombe; SPCC1919.09; -.
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 DR Pfam; PF01912; eIF6_1.
 DR ProDom; PD00680; eIF6_1.
 DR SMART; SMW0654; eIF6_1.
 KW Initiation factor; Protein biosynthesis; Phosphorylation.
 FT PHOSPHORYLATION (BY CK1)
 MOD_RES 174 174
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 DR Pfam; PF01912; eIF6_1.
 DR ProDom; PD00680; eIF6_1.
 DR SMART; SMW0654; eIF6_1.
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 MOD_RES 174 174
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 DR ProDom; PD00680; eIF6_1.
 DR SMART; SMW0654; eIF6_1.
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 DR ProDom; PD00680; eIF6_1.
 DR SMART; SMW0654; eIF6_1.
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 DR ProDom; PD00680; eIF6_1.
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 DR SMART; SMW0654; eIF6_1.
 DR Initiation factor; Protein biosynthesis; Phosphorylation (BY CK1)
 MOD_RES 174 174
 DR PHOSPHORYLATION (BY CK1)
 DR GenBank; SPCC1919.09; -.
 DR InterPro; IPR022

olfactory receptor gene families.";
 RRL Hum. Mol. Genet. 11:535-546 (2002).
 RN [3]
 RP ERRATUM.
 RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
 RA Trask B.J.;
 RA Young J.M., Friedman C., Williams E.M., Ross J.A., Tonnes-Priddy L.,
 RA Trask B.J.;
 CC -!- FUNCTION: Potential odorant receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 DR EMBL; AY073356; AAL61019.1; -;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PROSITE; PS000237; G-PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50052; G-PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT TRANSMEM 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 49 1 (POTENTIAL).
 FT TRANSMEM 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).
 FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 123 3 (POTENTIAL).
 FT DOMAIN 124 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 157 4 (POTENTIAL).
 FT DOMAIN 158 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 200 220 5 (POTENTIAL).
 FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 241 261 6 (POTENTIAL).
 FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 275 295 7 (POTENTIAL).
 FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 100 192 BY SIMILARITY.
 FT CARBOHYD 8 8 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 314 AA; 34549 MW; E143B2A1E0321BD9 CRC64;

Query Match 72.3%; Score 34; DB 1; Length 314;
 Best Local Similarity 72.8%; Pred. NO. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTI 9
 Db 41 TVSGNLTI 49

RESULT 8
 OR25_MOUSE STANDARD; PRT; 314 AA.
 ID OR25_MOUSE STANDARD;
 AC Q8VG07;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Putative olfactory receptor 204-10.
 GN MOR204-10.
 OS Mus musculus (Mouse).
 OC Bivalvia; Mollusca; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=1678863; PubMed=11802173;
 RA Zhang X., Firestein S.;

Query Match 72.3%; Score 34; DB 1; Length 314;
 Best Local Similarity 77.8%; Pred. NO. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTI 9
 Db 41 TVSGNLTI 49

RESULT 9
 OR28_MOUSE STANDARD; PRT; 314 AA.
 ID OR28_MOUSE STANDARD;
 AC Q8VG04;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DE Putative olfactory receptor 204-13.
 GN MOR204-13.

Mus musculus (Mouse). Chordata; Craniata; Vertebrata; Buteleostomi;
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1] _SEQUENCE FROM N.A. PubMed=2167863;
RX MEDLINE=2167863; PubMed=11802173;
RA Zhang X., Firestein S.;
RT "The olfactory receptor gene superfamily of the mouse.";
RL Nat. Neurosci. 5:124-133 (2002).
RN [2] _SEQUENCE FROM N.A. PubMed=21864068; PubMed=11875048;
RX MEDLINE=21864068; PubMed=11875048;
RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L.,
Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human
olfactory receptor gene families";
RL Hum. Mol. Genet. 11:535-546 (2002).
RN [3] _ERRATUM.
RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L.,
Trask B.J.;
RL Hum. Mol. Genet. 11:1683-1683 (2002).
CC !- FUNCTION: Potential odorant receptor.
CC !- SUBCELLULAR LOCATION: Integral membrane protein.
CC !- SIMILARITY: Belongs to Family 1 of G-protein coupled receptors.
CC

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or send an email to license@isb-sib.ch).

DR EMBL: AY73361; AA16102.1; -;
EMBL: AY217586; AAP70982.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
PRINTS: PR00237; GPCR_RHODOPSIN.
PROSITE: PS00237; G-PROTEIN_RECEP_F1_1;
PROSITE: PS00562; G-PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 29 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 78 2 (POTENTIAL).
FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 123 3 (POTENTIAL).
FT DOMAIN 124 136 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 137 157 4 (POTENTIAL).
FT TRANSMEM 158 199 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 200 220 5 (POTENTIAL).
FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 261 6 (POTENTIAL).
FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 275 295 7 (POTENTIAL).
FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).
FT DISULFID 100 192 BY SIMILARITY.
FT CARBOHYD 8 8 N-LINKED (GLCNAC, -) (POTENTIAL).
SQ SEQUENCE 314 AA; 34940 MW; 916122610A41A6EF CRC64;

Query Match 72.3%; Score 34; DB 1; Length 314;
Best Local Similarity 77.8%; Pred. No. 20;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTI 9
Db 41 TVSGNLTI 49

OB32_MOUSE STANDARD; PRT; 314 AA.
ID OR32_MOUSE
AC QBVFD2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Putative olfactory receptor 204-17.
GN MOR204_17.
OS Mus musculus (Mouse).
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID:10090;
RN [1] _SEQUENCE FROM N.A. PubMed=21864068; PubMed=11875048;
RX MEDLINE=21864068; PubMed=11875048;
RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L.,
Trask B.J.;
RT "Different evolutionary processes shaped the mouse and human
olfactory receptor gene families";
RL Hum. Mol. Genet. 11:535-546 (2002).
RN [3] _ERRATUM.
RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L.,
Trask B.J.;
RL Hum. Mol. Genet. 11:1683-1683 (2002).
CC !- FUNCTION: Potential odorant receptor.
CC !- SUBCELLULAR LOCATION: Integral membrane protein.
CC !- SIMILARITY: Belongs to Family 1 of G-protein coupled receptors.
CC

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or send an email to license@isb-sib.ch).

DR EMBL: AY073599; AAP70993.1; -;
DR EMBL: AY17598; AAP70993.1; -;
DR InterPro: IPR000276; GPCR_Rhodopsin.
DR Pfam: PF00001; 7tm_1; 1.
PRINTS: PR00237; GPCR_RHODOPSIN.
PROSITE: PS00237; G-PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
DR PROSITE: PS00262; G-PROTEIN_RECEP_F1_2; 1.
DR G-protein coupled receptor; Transmembrane; Glycoprotein;
KW Multigene family; Olfaction.
FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 29 49 1 (POTENTIAL).
FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 58 78 2 (POTENTIAL).
FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 123 3 (POTENTIAL).
FT DOMAIN 124 136 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 137 157 4 (POTENTIAL).
FT TRANSMEM 158 199 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 200 220 5 (POTENTIAL).
FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 241 261 6 (POTENTIAL).
FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 275 295 7 (POTENTIAL).
FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).
FT DISULFID 100 192 BY SIMILARITY.
FT CARBOHYD 8 8 N-LINKED (GLCNAC, -) (POTENTIAL).
SQ SEQUENCE 314 AA; 34744 MW; 35FF7679DB37FD7E CRC64;

Query Match 72.3%; Score 34; DB 1; Length 314;
Best Local Similarity 77.8%; Pred. No. 20;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

FT TRANSMEM 275 205 7 (POTENTIAL).
 FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 100 192 BY SIMILARITY.
 FT CARBOHYD 8 8 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CARBOHYD 268 268 N-LINKED (GLCNAC . .) (POTENTIAL).
 SQ SEQUENCE 314 AA; 34716 MW; 6DB1AEB76BBC795 CRC64;

RESULT 11
 ID OR33_MOUSE STANDARD; PRT; 314 AA.
 AC QBVFD1;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Putative olfactory receptor 204-18.
 DN MOR204-18.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TAXID=10090;

[1]
 RN SEQUENCE FROM N.A. MEDLINE=21676363; PubMed=11802173;
 RX MEDLINE=21676363; PubMed=11802173;
 RA Zhang X., Firestein S.;
 RA "The olfactory receptor gene superfamily of the mouse.";
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 5:124-133(2002).
 RN SEQUENCE FROM N.A. MEDLINE=2186408; PubMed=11875048;
 RX MEDLINE=2186408; PubMed=11875048;
 RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L.,
 RA Trask B.J.;
 RT "Differential evolutionary processes shaped the mouse and human
 olfactory receptor gene families.";
 RL Hum. Mol. Genet. 11:535-546(2002).
 RN ERATUM.
 RA Young J.M., Friedman C., Williams B.M., Ross J.A., Tonnes-Priddy L.,
 RA Trask B.J.;
 RL Hum. Mol. Genet. 11:1683-1683(2002).
 CC -!- FUNCTION: Potential odorant receptor.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
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CC EMBL: AY073600; AAL61263.1; -;
 DR EMBL: AY317600; AAP70995.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR PFAM: PF00001; 7tm_1; -;
 DR PRINTS: PRO0237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN_RECV_P1_1.
 DR PROSITE: PS0262; G-PROTEIN_RECV_P1_2.
 KW G-Protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 FT DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).
 FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 123 3 (POTENTIAL).
 FT DOMAIN 124 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 157 4 (POTENTIAL).
 FT DOMAIN 158 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 200 220 5 (POTENTIAL).
 FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 241 261 6 (POTENTIAL).
 FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 275 28 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 29 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).

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CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
 EMBL: AY317601; AAP70996; 1;
 DR EMBL: AY07783; AA61446; 1;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00061; 7tm; 1.
 DR PRINTS: PRO0237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN RECEP_P1_1; 1.
 DR PROSITE: PS00237; G-PROTEIN RECEP_P1_2; 1.
 DR PROSITE: PS00262; G-PROTEIN TRANSMEM; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 29 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).
 FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 123 3 (POTENTIAL).
 FT DOMAIN 124 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 157 4 (POTENTIAL).
 FT DOMAIN 158 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 200 220 5 (POTENTIAL).
 FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 241 261 6 (POTENTIAL).
 FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 275 295 7 (POTENTIAL).
 FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 100 192 BY SIMILARITY.
 CARBOND 8 N-LINKED (GLCNAC, *.) (POTENTIAL).
 SEQUENCE 314 AA; 34953 MW; 99D8516859F6B54D CRC64;
 Query Match 72.3%; Score 34; DB 1; Length 314;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTI 9
 .Db 41 TVSGNLTI 49

RESULT 15
 OR22_MOUSE STANDARD PRT; 316 AA.
 AC Q8VG13;
 ID OR22_MOUSE
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Putative olfactory receptor 204-7.
 GN MOR204-7.
 OS *Mus musculus* (Mouse).
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI TaxID:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21864068; PubMed=11875048;
 RX Zhang X.; Firestein S.;
 RA Young J.M.; Friedman C.; Williams E.M.; Ross J.A.; Tonnes-Priddy L.;
 RA Trask B.J.;
 RT "The olfactory receptor gene superfamily of the mouse.";
 RL Nat. Neurosci. 5:124-133 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21864068; PubMed=11875048;
 RX Young J.M.; Friedman C.; Williams E.M.; Ross J.A.; Tonnes-Priddy L.;
 RA Trask B.J.;
 RT "Different evolutionary processes shaped the mouse and human
 olfactory receptor gene families.";
 RL Hum. Mol. Genet. 11:535-546 (2002).
 RN [3]
 RP ERRATUM.
 RA Young J.M.; Friedman C.; Williams E.M.; Ross J.A.; Tonnes-Priddy L.;
 RA Trask B.J.;
 RL Hum. Mol. Genet. 11:1693-1694 (2002).
 -!- FUNCTION: Potential odorant receptor.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 EMBL: AY073352; AA61015; 1;
 DR EMBL: AY317615; AAP7105; 1;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm; 1.
 DR PRINTS: PR0023; GPCR_RHODOPSIN.
 DR PROSITE: FS00237; G-PROTEIN RECEP_F1; G-PROTEIN RECEP_F1-2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Multigene family; Olfaction.
 DOMAIN 1 28 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 29 49 1 (POTENTIAL).
 FT DOMAIN 50 57 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 58 78 2 (POTENTIAL).
 FT DOMAIN 79 102 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 103 123 3 (POTENTIAL).
 FT DOMAIN 124 136 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 137 157 4 (POTENTIAL).
 FT DOMAIN 158 199 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 200 220 5 (POTENTIAL).
 FT DOMAIN 221 240 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 241 261 6 (POTENTIAL).
 FT DOMAIN 262 274 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 275 295 7 (POTENTIAL).
 FT DOMAIN 296 314 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 100 192 BY SIMILARITY.
 FT TRANSMEM 300 320 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 321 341 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 342 361 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 362 381 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 382 401 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 402 421 CYTOPLASMIC (POTENTIAL).
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 FT DOMAIN 602 621 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 622 641 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 642 661 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 662 681 N-LINKED (GLCNAC, *.) (POTENTIAL).
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 FT TRANSMEM 5782 5801 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 5802 5821 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 5822 5841 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 5842 5861 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 5862 5881 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 5882 5901 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 5902 5921 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 5922 5941 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 5942 5961 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 5962 5981 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 5982 6001 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 6002 6021 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 6022 6041 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 6042 6061 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 6062 6081 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 6082 6101 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 6102 6121 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 6122 6141 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 6142 6161 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 6162 6181 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 6182 6201 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 6202 6221 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 6222 6241 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 6242 6261 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 6262 6281 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 6282 6301 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 6302 6321 N-LINKED (GLCNAC, *.) (POTENTIAL).
 FT DOMAIN 6

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OX: protein - protein search, using sw model

Run on: June 22, 2004, 08:47:17 ; Search time 24 Seconds

{without alignments}

131.466 Million cell updates/sec

Title: US-09-529-206D-4_COPY_127_136

Perfect score: 47

Sequence: 1 TVSGNLTIR 10

Scoring table: BLOSUM62

Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

SPREMBI_25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteria:*
- 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	39	83.0	142	4 Q9NY13	Q9ny13 homo sapien
2	38	80.9	180	4 Q9Y473	Q9y473 homo sapien
3	37	78.7	250	16 Q8G743	Q8g743 bifidobacterium
4	36	76.6	245	9 O64327	O64327 bacteriophage
5	36	76.6	318	16 O8EA04	O8ea04 shewanella
6	36	76.6	352	13 Q9HY4	Q9hy4 lampetra fl
7	36	76.6	450	16 Q9RU1	Q9ru1 streptomyces
8	35	74.5	144	16 Q8A976	Q8a976 bacteroides
9	35	74.5	335	16 Q932P0	Q932p0 staphylococcus
10	35	74.5	335	16 Q99VV7	Q99vv7 staphylococcus
11	35	74.5	336	16 Q8CQ35	Q8cq35 staphylococcus
12	35	74.5	674	13 Q9PT83	Q9pt83 xenopus lae
13	35	74.5	674	13 Q9PT82	Q9pt82 xenopus lae
14	35	74.5	742	5 Q9VS06	Q9vs06 drosophila
15	35	74.5	742	5 Q8T4D0	Q8t4d0 drosophila
16	35	74.5	907	5 Q9NGG0	Q9ngg0 drosophila

Title:	US-09-529-206D-4_COPY_127_136
Perfect score:	47
Sequence:	1 TVSGNLTIR 10
Scoring table:	BLOSUM62
Gapext:	0.5
Minimum DB seq length:	0
Maximum DB seq length:	2000000000
Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing First 45 summaries
Database :	
1: sp_archaea:*	
2: sp_bacteria:*	
3: sp_fungi:*	
4: sp_human:*	
5: sp_invertebrate:*	
6: sp_mammal:*	
7: sp_mhc:*	
8: sp_organelle:*	
9: sp_phage:*	
10: sp_plant:*	
11: sp_rabbit:*	
12: sp_virus:*	
13: sp_vertebrate:*	
14: sp_unclassified:*	
15: sp_rvirus:*	
16: sp_bacteria:*	
17: sp_archaea:*	

ALIGNMENTS

RESULT 1	Q9NY13	PRELIMINARY	PRT;	142 AA.
ID	Q9NY13	AC	Q9NY13;	
AC	Q9NY13;	DT	01-OCT-2000 (TREMBLrel. 15, Created),	
		DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
		DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)	
DB		DB	Hypothetical Protein (Fragment).	
GN		GN	LAGE-2.	
OS		OS	Homo sapiens (Human).	
OC		OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC		OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	
NCBI_TaxID	9606;	NCB1_TaxID	9606;	
RN	[1]	RN	SEQUENCE FROM N.A.	
RP		RP	Leche B.G.;	
RA		RA	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	
RL		RL	EMBL: AJ227578; CAB7645.1; -.	
DR		DR		
KW		KW	Hypothetical Protein.	
NON_TER	1	SEQUENCE	142 AA;	13895 MW;
				27EBB922AC4ACCT7B CRC64;
FT		Query Match	83.0%	Score 39;
		Best Local Similarity	88.9%	DB 4;
		Matches	8;	Length 142;
		Conservative	1;	
		Mismatches	0;	
		Indels	0;	
		Gaps	0;	
Qy		1 TVSGNLTIR 9		
		:		
Db		101 TVSGNLTIR 109		
		:		
RESULT 2				
Q9479		PRELIMINARY	PRT;	180 AA.
ID	Q9479	AC	Q9479;	
		DT	01-NOV-1999 (TREMBLrel. 12, Created),	
		DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)	
		DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)	
		DR	LAGE-2 protein (Cancer/testis antigen 2).	

GN LAGE1.	AC 064327;	AC 064327;
OS Homo sapiens (Human).	DT 01-AUG-1998 (TREMBLrel. 07; Created)	DT 01-AUG-1998 (TREMBLrel. 07; Last sequence update)
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteostomi;	DT 01-AUG-1998 (TREMBLrel. 07; Last sequence update)	DT 01-OCT-2003 (TREMBLrel. 25; Last annotation update)
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo;	DE GPB13.	DE GPB13.
OX NCBI_TaxID=9606;	GN GENB_13.	GN GENB_13.
RN [1]	OS Bacteriophage N15.	OS Bacteriophage N15.
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
TISSUE=Me lanoma;	OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;	RA Hendrix R.W., Ravin V.K., Casjens S.R., Ford M.E., Ravin N.V.,
MEDLINEB=9325550; PubMed=10399963;	OC Lambda-like viruses.	RA Smirnov I.K.;
RA Arnouze C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.,	RP Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.	RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RT "unexpected translation product of LAGE1.";	DR AF064539; AAC19050.1; -.	DR AF064539; AAC19050.1; -.
RL Int. J. Cancer 82:442-448(1999).	DR P13099; T13099.	DR P13099; T13099.
RP SEQUENCE FROM N.A.	DR InterPro: IPR003964; Invasion_intimin.	DR InterPro: IPR003964; Invasion_intimin.
RA Aradhy S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,	DR PFAM: PF02368; Big_2_1.	DR PFAM: PF02368; Big_2_1.
RA Patil H., Ciccidiola A., Kenrick S., Platzter M., D'Urso M.,	DR SMART: SM00635; BID_1; 1.	DR SMART: SM00635; BID_1; 1.
RA Nelson D.L.;	DR SEQUENCE 245 AA; 25571 MW; 2CC941997C103FD3 CRC64;	DR SEQUENCE 245 AA; 25571 MW; 2CC941997C103FD3 CRC64;
RT "Multiple pathogenic and benign genomic rearrangements occur at a 35- kb duplication involving the NEMO and the LAGE2 genes.";	Query Match Score 76.6%; Best Local Similarity 77.8%; Pred. No. 40; Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;	Query Match Score 76.6%; Best Local Similarity 77.8%; Pred. No. 40; Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;
RA Hum. Mol. Genet. 10:0-0(2001).	Qy 1 TVSGNLTI 9	Qy 1 TVSGNLTI 9
RL EMBL: AF273315; CAI10194.1; -.	Db 209 TVSGNLTI 217	Db 209 TVSGNLTI 217
DR EMBL: AF273315; CAI10194.1; -.	RESULT 5	RESULT 5
SEQUENCE 180 AA; 18236 MW; 9077FAP953543A25 CRC64;	Q8EAQ4	Q8EAQ4
Query Match Score 80.9%; Best Local Similarity 80.0%; Pred. No. 11; Matches 8; Conservative 8; Mismatches 1; Indels 1; Gaps 0;	ID Q8EAQ4	ID Q8EAQ4
DR SEQUENCE 180 AA; 18236 MW; 9077FAP953543A25 CRC64;	AC Q8EAQ4;	AC Q8EAQ4;
Qy 1 TVSGNLTI 10	DT 01-MAR-2003 (TREMBLrel. 23; Created)	DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)
Db 127 TVSGNLTI 136	DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)
RESULT 3	DB 9; Length 245;	DB 9; Length 245;
Q8G743	PRELIMINARY;	PRELIMINARY;
AC Q8G743	PRRT; 250 AA.	PRRT; 318 AA.
DR Q8G743; 23. Created)	RC	RC
DT 01-MAR-2003 (TREMBLrel. 23; Last sequence update)	RC STRAIN=NMR-1;	RC STRAIN=NMR-1;
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	RA Heideberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward R., Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M., Methe B., Daugherty S.,	RA Heideberg J.P., Paulsen I.T., Nelson K.B., Gaidos E.J., Nelson W.C., Read T.D., Eisen J.A., Seshadri R., Ward R., Clayton R.A., Meyer T., Tsapin A., Scott J., Beaman M., Methe B., Daugherty S.,
DT 01-MAR-2003 (TREMBLrel. 23; Last annotation update)	RA Durkin R.J., Koleny J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,	RA Durkin R.J., Koleny J.F., Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M., Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
DB Possible cobyrinic acid synthase CobQ.	RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., Feldblyum T.V., "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";	RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M., Feldblyum T.V., "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";
GN BL0129.	RA Shewanella Nat. Biotechnol. 20:1118-1123 (2002).	RA Shewanella Nat. Biotechnol. 20:1118-1123 (2002).
OS Bifidobacterium longum.	DR EMBL: AE013817; ZAN55819.1; -.	DR EMBL: AE013817; ZAN55819.1; -.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;	KW Hypothetical protein; Complete proteome.	KW Hypothetical protein; Complete proteome.
OC Bifidobacteriaceae; Bifidobacterium.	SEQUENCE 3218 AA; 34113 MW; 0A037165033B6FCF CRC64;	SEQUENCE 3218 AA; 34113 MW; 0A037165033B6FCF CRC64;
OX NCBI_TaxID=216816;	Qy 1 TVSGNLT 8	Qy 1 TVSGNLT 8
RN [1]	RESULT 4	RESULT 4
RP SEQUENCE FROM N.A.	DR 064327;	DR 064327;
STRAIN=NCC 2705;	DR SO3812; -.	DR SO3812; -.
MEDLINEB=2229477; PubMed=12381787;	KW Hypothetical protein; Complete proteome.	KW Hypothetical protein; Complete proteome.
RA Scheifele M.A., Karmirantzou M., Snel B., Vilanova D., Berger B., Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M., Pridmore R.D., Arigoni P., "The genome sequence of Bifidobacterium longum reflects its adaptation to the human gastrointestinal tract.";	Qy 1 TVSGNLT 10	Qy 1 TVSGNLT 10
RA PROC. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).	DB 21 SGVNLT 28	DB 21 SGVNLT 28
DR EMBL: AB014661; AN24266.1; -.	DR 153 TVSGNLT 160	DR 153 TVSGNLT 160
KW Complete proteome.	DR EMBL: AB013817; ZAN55819.1; -.	DR EMBL: AB013817; ZAN55819.1; -.
SEQUENCE 250 AA; 27653 MW; 757795A609689CF CRC64;	Query Match Score 78.7%; Best Local Similarity 87.5%; Pred. No. 25; Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;	Query Match Score 78.7%; Best Local Similarity 87.5%; Pred. No. 52; Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Query Match Score 78.7%; Best Local Similarity 87.5%; Pred. No. 25; Matches 7; Conservative 7; Mismatches 0; Indels 0; Gaps 0;	Qy 3 SGNLTIR 10	Qy 3 SGNLTIR 10
DR EMBL: AB013817; ZAN55819.1; -.	Db 21 SGVNLT 28	Db 21 SGVNLT 28

RESULT 6

Q9HY4 PRELIMINARY; PRT; 352 AA.
 AC Q9HY4; PRELIMINARY; PRT; 352 AA.
 DT 01-MAY-1999 (TREMBREL 10, Created)
 DT 01-JUN-2003 (TREMBREL 24, Last sequence update)
 DT Putative odorant receptor LQR1.
 DE Putative odorant receptor LQR1.
 OS Lampetra fluvialis (River Lamprey).
 EUkaryota: Metazoa: Chordata: Craniata: Vertebrata: Hyperoartia;
 OC Petromyzontiformes: Petromyzontidae: Lampetra.
 OC NCBI_TaxID=7748;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Olfactory organ;
 RA Berglund A., Dryer L.;
 RA "A novel family of ancient vertebrate odorant receptors.";
 RL J. Neurobiol. 0:0 (1998).
 CC --: SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
 CC --: SIMILARLY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 EMBL: AF069546; AAC82381.1;
 DR GO:0016021; C: integral to membrane; IBA.
 DR GO:0004872; F: receptor activity; IBA.
 DR GO:0001584; F: rhodopsin-like receptor protein signalin. . .; IBA.
 DR GO:0007186; P: G-protein coupled receptor protein signalin. . .; IBA.
 DR IPRO00276; GPCR_Rhodopsn.
 PFam: PF00001; 7tm 1; 1.
 PRINTS: PR00237; GPRORHODOPSN.
 DR PROSITE; PS00237; G PROTEIN RECEPTOR_F1_1; 1.
 DR PROSITE; PS05222; G PROTEIN RECEPTOR_F1_2; 1.
 DR PROSITE; PS05222; G PROTEIN RECEPTOR_Transmembrane.
 KW SEQUENCE 352 AA; 40276 MW; 6366743DFFA9P4B CRC64;
 + SQ

Query Match 76.6%; Score 36; DB 13; Length 352;
 Best Local Similarity 88.9%; Preg. No. 58;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 TVSGNLTI 9
 Db 45 TVVGNLTI 53

Query Match 76.6%; Score 36; DB 16; Length 450;
 Best Local Similarity 80.0%; Preg. No. 75;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 TVSGNLTIR 10
 Db 405 TNSGNVMTVR 414

RESULT 7

Q9R191 PRELIMINARY; PRT; 450 AA.
 AC Q9R191; PRELIMINARY; PRT; 450 AA.
 DT 01-MAY-2000 (TREMBREL 13, Created)
 DT 01-MAY-2000 (TREMBREL 13, Last sequence update)
 DT 01-OCT-2003 (TREMBREL 25, Last annotation update)
 DB Secreted endo-1,4-beta-xylanase (EC 3.2.1.8).
 GN OS SCO0674 OR SCSP91_34C.
 OS Streptomyces coelicolor.
 OC Bacteria: Actinobacteridae: Streptomyctaceae; Actinomycetales;
 OC Streptomyces; Streptomyctaceae; Streptomyces
 OC NCBITaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2);
 RA Oliver K., Harris D.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC THOMSON N.R., Parkhill J., Barrell B.G., Rajandream M.A.; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2);
 RX MEDLINE=97000351; PubMed=844346;
 RA Redenbach M., Kieser H.M., Danapaita D., Eichner A., Cullum J., Kinashi F., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map for

the 8 Mb Streptomyces coelicolor A3 (2) chromosome.";
 RL Mol. Microbiol. 21:77-96 (1996).

[4]

RP SEQUENCE FROM N.A.
 RC STRAIN=A3 (2) / MI:45;
 RX MEDLINE=21995410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Crokin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S., Rajbhandary E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Taylor K., Warren T., Wietzorek A., Woodward B.G., Parkhill J., Hopwood D.A.; "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3 (2).";
 RT Nature 417:141-147 (2002).
 RL EMBL; AL939106; CAB61191.1; -
 HSSP; P07986; 1EXP.
 GO: GO-0004553; F: hydrolase activity, hydrolyzing O-glycosyl . . .; IBA.
 DR GO:0005975; P: carbohydrate metabolism; IBA.
 DR InterPro; IPR01919; Baculose-bind.
 DR InterPro; IPR008965; Cellulose-bind.
 DR InterPro; IPR00000; Glyco_Hydro_10.
 DR Pfam; PF00553; CBM 2, 1.
 DR PR00331; Glyco_Hydro_10; 1.
 DR PRINTS; PR00134; GLYHTRLASE10.
 SMART; SM00537; CBD_II; 1.
 SMART; SM00613; Glyco_10.
 DR PROSITE; PS00591; GLYCOSIDASE_HYDROL_F10; 1.
 KW Glycosidase; Hydrolase; Xylan degradation; Complete proteome.
 SQ SEQUENCE 450 AA; 41090 MW; B2FF6A36EC29B6AE CRC64;

RESULT 8

Q9A9JB PRELIMINARY; PRT; 144 AA.
 AC Q9A9JB; PRELIMINARY; PRT; 144 AA.
 DT 01-JUN-2003 (TRIMBLrel. 24, Created)
 DT 01-JUN-2003 (TRIMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TRIMBLrel. 25, Last annotation update)
 DB Lipoprotein, function unknown.
 GN BM0817.
 OS Bacteroides thetaiotaomicron.
 OC Bacteroides; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidiaceae; Bacteroides.
 OC NCBITaxID=818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VP1-5482 / ATCC 29148;
 RX MEDLINE=22550858; PubMed=12663928;
 RA Chiang H.-C., Bjurzell M.K., Hammrod J., Deng S., Carmichael J., Xu J., Hooper L.V., Gordon J.I.; "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis.";
 RT Science 299:2074-2076 (2003).
 DR EMBL; AE016329; AA07524; 1; -
 DR InterPro; IPR002298; NIPB
 DR InterPro; IPR000437; Prok_lipoprot_S.
 DR Pfam; PF04170; NIPB; 1.
 DR PROSITE; PS00013; PROKAR_LIPOPOTREIN; 1.
 KW Complete proteome.
 SQ SEQUENCE 144 AA; 15781 MW; AB2835887FE6978B CRC64;

Query Match

74.5%; Score 35; DB 16; Length 144;

Best Local Similarity 60.0%; Pred. No. 36; Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 96 TLEGNLTIR 105

RESULT 9
Q932F0 PRELIMINARY; PRT; 335 AA.

AC Q932F0; Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
HYPOTHETICAL PROTEIN SAV0664.

GN SAV0664.

OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699).

OX Bacteria; Firmicutes; Bacillales; Staphylococcaceae; NCBI_TaxID=158878;

RN SEQUENCE FROM N.A.; MEDLINE=21311952; PubMed=11418146;

RX Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Kobayashi K., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K., "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*," Lancet 357:1225-1240 (2001).

RN SEQUENCE FROM N.A.

AC Q932F0; PRELIMINARY; PRT; 335 AA.

DR GO:0016020; C:membrane; IEA.

DR GO:0005315; F:inorganic phosphate transporter activity; IEA.

DR GO:0006817; P:phosphate transport; IEA.

DR InterPro; IPR011204; Phos_transporter.

DR PF01384; PHO4; 1.

KW Hypothetical protein; Complete proteome.

SEQNECE 335 AA; 35604 MW; 9155CA83343FD628 CRC64;

Query Match 74.5%; Score 35; DB 16; Length 335; Best Local Similarity 70.0%; Pred. No. 89; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 245 TVGGNIMKIR 254

RESULT 10
Q99VV7 PRELIMINARY; PRT; 335 AA.

AC Q99VV7; Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

HYPOTHETICAL PROTEIN SA0019 (MW0626 protein).

GN SA0019 OR MW0626.

OS *Staphylococcus aureus* (strain N315), and *Staphylococcus aureus* (strain MW2).

OX Bacteria; Firmicutes; Bacillales; Staphylococcaceae; NCBI_TaxID=158879; 196620;

RN SEQUENCE FROM N.A.

RC STRAIN=N315;

RX MEDLINE=21311952; PubMed=11418146;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I., Cui L., Ouchi A., Aoki K.I., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K., "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*," Lancet 357:1225-1240 (2001).

RN SEQUENCE FROM N.A.

RC STRAIN=MW2;

RX MEDLINE=2240717; PubMed=12044378;

RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K., "Genome and virulence determinants of high virulence community-acquired MSSA," Lancet 359:1819-1827 (2002).

DR AP004131; BAB41952; 1.

DR EMBL; AP004824; BAB94491; 1.

DR PIR; A89837; A89837.

DR GO; GO-0005315; C:membrane; IEA.

DR GO; GO-0005315; F:inorganic phosphate transporter activity; IEA.

DR InterPro; IPR01204; Phos_transporter.

DR PF01384; PHO4; 1.

KW Hypothetical protein; Complete proteome.

SEQNECE 335 AA; 35811 MW; 5918CA94BC9A3D99 CRC64;

Query Match 74.5%; Score 35; DB 16; Length 336; Best Local Similarity 70.0%; Pred. No. 89; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 245 TVGGNIMKIR 254

RESULT 11
Q8CQ35 PRELIMINARY; PRT; 336 AA.

AC Q8CQ35; Created)

DR GO:0016020; C:membrane; IEA.

DR GO:0005315; F:inorganic phosphate transporter activity; IEA.

DR GO:0006817; P:phosphate transport; IEA.

DR InterPro; IPR01204; Phos_transporter.

DR PF01384; PHO4; 1.

KW Complete proteome.

SEQUENCE 336 AA; 35811 MW; 5918CA94BC9A3D99 CRC64;

Query Match 74.5%; Score 35; DB 16; Length 336; Best Local Similarity 70.0%; Pred. No. 89; Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TVSGNLTIR 10
Db 245 TVGGNIMKIR 254

RESULT 12
Q9P183

RA Zheng X.H.; Zhong F.N.; Zhong W.; Zhou X.; Zhu S.; Zhu X.; Smith H.O.,
RA Gibbs R.A.; Myers E.W.; Rubin G.M.; Venter J.C.; "The genome sequence of *Drosophila melanogaster*.";
RT "The genome sequence of *Drosophila melanogaster*.";
RL Science 287:2135-2139 (2000).
DR SMBL; AB013560; AAF50630.1; -.
DR FlyBase; FBgn0035724; CG10064.
DR InterPro; IPR001680; WD40.
DR Pfam; PF01400; WD40; 10.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00320; WD40; 8.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 4.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD_repeat.
SQ SEQUENCE 742 AA; 81994 MW; B6F3210064859141 CRC64;
Query Match 74.5%; Score 35; DB 5; Length 742;
Best Local Similarity 66.7%; Pred. No. 2.1e+02; Length 742;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 VSGNLTIR 10
Db 154 ISGNALTVR 162

RESULT 15
Q8T4D0 PRELIMINARY; PRT; 742 AA.
ID Q8T4D0; AC; DT 01-JUN-2002 (TREMBLrel. 21; Created); DT 01-JUN-2002 (TREMBLrel. 21; Last sequence update); DT 01-JUN-2003 (TrEMBLrel. 24; Last annotation update); DE AT0371P.
GN CG10064.
OS *Drosophila melanogaster* (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
* OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Epipharyngea; Drosophilidae; Drosophila.
NCBI TaxID:7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M.; Brookstein P.; Hong L.; Agbayani A.; Carlson J.; Frise E.;
RA Chame M.; Chavez C.; Dorsett V.; Drensek D.; Farfan D.; Liao G.;
RA George R.; Gonzalez M.; Guarin H.; Kronmiller B.; Li P.; Paragas V.; Park S.;
RA Miralda A.; Mungall C.J.; Nunoco J.; Pacleb J.; Paragas V.; Park S.;
RA Patel S.; Phouanenavong S.; Wan K.; Yu C.; Lewis S.E.; Rubin G.M.;
RA Celinker S.;
RL Submitted (MAR 2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY059248; AY059986.1; CG10064.
DR FlyBase; FBgn0035724; CG10064.
DR InterPro; IPR001680; WD40.
DR Pfam; PF00400; WD40; 10.
DR PRINTS; PR00320; GPROTEINBRPT.
DR SMART; SM00320; WD40; 10.
DR PROSITE; PS00678; WD_REPEATS_1; 1.
DR PROSITE; PS50082; WD_REPEATS_2; 4.
DR PROSITE; PS50294; WD_REPEATS_REGION; 1.
KW Repeat; WD_repeat.
SQ SEQUENCE 742 AA; 82012 MW; BC13210535849140 CRC64;
Query Match 74.5%; Score 35; DB 5; Length 742;
Best Local Similarity 66.7%; Pred. No. 2.1e+02; Length 742;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 2 VSGNLTIR 10
Db 154 ISGNALTVR 162

Search completed: June 22, 2004, 08:53:26
Job time : 27 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	107	100.0	20	RAY05979	Aay05979 Human can
2	107	100.0	180	AAW62584	Aaw62584 Cancer as
3	107	100.0	180	AAW62665	Aaw62665 Human NY-
4	107	100.0	180	AAY05965	Aay05965 Human can
5	107	100.0	180	AAY52430	Aay52430 Human tum
6	107	100.0	180	AAY70862	Aay70862 Human tum
7	107	100.0	180	AA003154	Aao03154 Human oes
8	107	100.0	180	ABB63946	Aab63946 Human NY-
9	107	100.0	180	AAG67164	Aag67164 Anirno aci
10	107	100.0	180	AAU01535	Aau01535 Human NY-
11	107	100.0	180	AAE07214	Aae07214 Human NY
12	107	100.0	180	AAU84818	Aau84818 Human NYN
13	107	100.0	180	AAU11543	Aau11543 Human tum
14	107	100.0	180	ABR58672	ABr58672 Human can
15	107	100.0	180	ABR48210	ABr48210 Human bla
16	107	100.0	180	ABU56508	ABu56508 Lung canc
17	107	100.0	180	ABU56694	ABu56694 Lung canc
18	107	100.0	180	ABP74198	ABp74198 Human NY-
19	107	100.0	180	ABR33438	ABr33438 Human NY-
20	107	100.0	180	ADC09576	ADC09576 Human NY-ESO-1
21	107	100.0	180	ADD35568	ADD35568 Human NY-
22	107	100.0	180	ADD25510	ADD25510 Banding d
23	107	100.0	397	ARE13122	ARE13122 Human NY-ESO-1C
24	102	95.3	5	AAU85105	AAu85105 Human NYN
25	102	95.3	3541	AAU85130	AAu85130 Human mei

or tumour antigen; antibodies reacting with a CRG-3 cancer peptide, useful in diagnostic and detection assays; and methods for preventing or inhibiting cancer by administering a cancer peptide, with or without an HLA molecule. The cancer peptides form part of, or are derived from, cancers such as primary or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine cancer, cervical cancer, bladder cancer, kidney cancer and adenocarcinomas such as breast, prostate, ovarian, pancreatic and thyroid cancers. Melanoma is treated by inducing cancer-specific T cells in vitro for subsequent return to a patient.

Sequence 20 AA;

Query Match 100.0%; Score 107; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.3e-06; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 RGPRGAGAARASGPGGAPR 20
Db 1 RGPRGAGAARASGPGGAPR 20

RESULT 2

AAW62584 Standard; protein; 180 AA.
XX

AAW62584;

AC 17-SEP-1998 (first entry)

DE Cancer associated antigen NY-ESO-1.

XX Cancer associated antigen; NY-ESO-1; regression; progression; onset; cancer; treatment; diagnosis.
KW XX Homo sapiens.

OS XX WO9832055-A1.

PH XX Key-Location/Qualifiers

FT Misc-difference 7 /note= "Potential myristylation site"

FT Misc-difference 9 /note= "potential myristylation site"

FT Misc-difference 11 /note= "potential phosphorylation site"

FT Misc-difference 98 /note= "potential phosphorylation site"

FT Misc-difference 134 /note= "potential phosphorylation site"

FT Misc-difference 138 /note= "potential phosphorylation site"

FT WO9814464-A1.

XX 09-APR-1998.

PP 15-SEP-1997; 97WO-US016335.

PR 03-OCT-1996; 96US-00725182.

PA (LUDWIG INST CANCER RBS.

XX PI Chen Y, Scanlan M, Gure A, Old LJ, Jager B, Knuth A;

PI Drijfhout JW;

XX DR 1998-286417/25.

DR N-PSDB; AAV38566.

XX New isolated cancer associated antigen - is used to develop products for the diagnosis and treatment of cancers and for monitoring cancer therapy.
PT XX PS Claim 8; Fig 3; 49PP; English.
XX The present sequence represents a cancer associated antigen. The clone CC from which the DNA sequence is obtained is designated NY-ESO-1. The CC specification described a method for determining regression, progression CC of onset of a cancerous condition, comprising monitoring a sample from a CC patient with the cancerous condition for a parameter selected from NY-ESO CC -1 protein, a peptide derived from NY-ESO-1 protein and cyolytic T cells CC specific for the peptide and an MHC molecule with which it is non-covalently CC complexes. Methods for the treatment of a cancerous condition are also CC described. The NY-ESO-1 protein and peptides derived from it can be used CC for diagnosis and treatment of cancers and to monitor the efficacy of a CC therapeutic regime.
XX SQ Sequence 180 AA;
Query Match 100.0%; Score 107; DB 2; Length 180;
Best Local Similarity 100.0%; Pred. No. 5.6e-05; Mismatches 0; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

Qy 1 RGPRGAGAARASGPGGAPR 20
Db 43 RGPRGAGAARASGPGGAPR 62

RESULT 3

AAW69665

ID AAW69665 standard; protein; 180 AA.

XX AAW69665;

AC 27-OCT-1998 (first entry)

DE Human NY-ESO-1 protein sequence, formerly known as LL-1.2 clone.
XX Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour.
XX Homo sapiens.
OS XX WO9832055-A1.

PN XX

XX 30-JUL-1998.

DD XX 98WO-US001445.

PP XX 27-JAN-1998;

PR XX 27-JAN-1997;

PA (LUDWIG INST CANCER RES.

XX XX Lethe B, Lucas S, De Smet C, Godelaine D, Boon-Falleur T;

PI XX DR WPI: 1998-427951/36.

DR N-PSDB; AAV50348.

XX XX New isolated LAGE-1 tumour associated nucleic acids - used to develop PT products for the diagnosis and treatment of LAGE-1 associated disorders. PT particularly tumours.
XX XX Example 2; Page 57-58; 73PP; English.

XX The present sequence represents human NY-ESO-1, formerly known as LL-1.2 CC clone, which is used in an example from the present invention which CC describes LAGE-1 tumour associated protein (TAP). The present invention CC also describes: (1) a method for treating a subject with a disorder CC characterised by expression of a LAGE-1 nucleic acid molecule or an CC expression product, comprising administering to the subject the disorder, where the cycolytic T cells to ameliorate the disorder, and a LAGE-1 TAP or an CC immunogenic fragment; (2) a method for treating a subject with a disorder CC characterised by expression of a LAGE-1 nucleic acid molecule or an CC expression product, comprising administering a LAGE-1 TAP or an CC immunogenic fragment to ameliorate the disorder; and (3) a method for CC selectively enriching a population of T cells with cycolytic T cells CC specific for a LAGE-1 TAP comprising contacting an isolated population of CC T cells with an agent presenting a complex of a LAGE-1 TAP or an CC immunogenic fragment and a HLA presenting molecule to selectively enrich

XX	SQ	Sequence 180 AA;
	Query Match	100.0%
	Best Local Similarity	100.0%
	Matches 20;	Conservative 0;
	Mismatches 0;	Indels 0;
	Gaps 0;	
Qy		1 RGPGRAGAARASGPGGAPR 20
Db		43 RGPGRAGAARASGPGGAPR 62
RESULT 5		
	AAY52430	Human tumour antigen NY-ESO-1.
	XX	
	DE	
	XX	
	XX	Cancer; tumour; antigen; MHC; major histocompatibility complex; T-cell; cytotoxic; helper; stimulation; proliferation; treatment; diagnosis;
	KW	prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
	KW	hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
	XX	
	XX	
	OS	Homo sapiens.
	XX	
	PH	
	Peptide	Location/Qualifiers
	FT	44. .53 "Peptide presented by MHC Class I HLA-B7"
	Peptide	60. .69 "Peptide presented by MHC Class I HLA-B7"
	FT	60. .68 "Peptide presented by MHC Class I HLA-B7"
	Peptide	63. .72 "Peptide presented by MHC Class I HLA-B7"
	FT	79. .88 "Peptide presented by MHC Class I HLA-B7"
	Peptide	79. .87 "Peptide presented by MHC Class I HLA-B7"
	FT	82. .91 "Peptide presented by MHC Class I HLA-B7, and HLA-B35"
	FT	82. .90 "Peptide presented by MHC Class I HLA-A1"
	Peptide	83. .91 "Peptide presented by MHC Class I HLA-A1"
	FT	84. .92 "Peptide presented by MHC Class I HLA-B44"
	FT	87. .96 "Peptide presented by MHC Class I HLA-B7, and HLA-B35"
	FT	88. .96 "Peptide presented by MHC Class I HLA-A1"
	Peptide	96. .104 "Peptide presented by MHC Class I HLA-B44"
	FT	100. .108 "Peptide presented by MHC Class I HLA-B7"
	Peptide	102. .110 "Peptide presented by MHC Class I HLA-B44"
	FT	107. .116 "Peptide presented by MHC Class I HLA-B44"
	FT	110. .118 "Peptide presented by MHC Class I HLA-A24"
	Peptide	113. .122 "Peptide presented by MHC Class I HLA-B52"
	FT	113. .121 "Peptide presented by MHC Class I HLA-B7 and HLA-B52"
	FT	115. .124 "Peptide Presented by MHC Class I HLA-B7"
	Peptide	115. .124 "Peptide Presented by MHC Class I HLA-A3"
	FT	

FT	Peptide	118. -126	Peptide presented by MHC Class I HLA-B35"	Best Local Similarity 100 %; Pred. No. 5.6e-05; Mismatches 0; Indels 0; Gaps 0;
FT	Peptide	124. -133	/note= "Peptide presented by MHC Class I HLA-B52"	Qy 1 RGPGRGAAARASPGGGAPR 20
FT	Peptide	125. -133	/note= "Peptide presented by MHC Class I HLA-B24"	Db 43 RGPGRGAAARASPGGGAPR 62
FT	Peptide	128. -147	/note= "Peptide presented by MHC Class I HLA-B8"	
FT	Peptide	139. -147	/note= "Peptide presented by MHC Class I HLA-B7"	RESULT 6
FT	Peptide	145. -153	/note= "Peptide presented by MHC Class I HLA-A24 and HLA-B52"	AAY70862
FT	Peptide	153. -162	/note= "Peptide presented by MHC Class I HLA-B52"	ID AAY70862 standard; protein; 180 AA; XX
FT	Peptide	154. -163	/note= "Peptide presented by MHC Class I HLA-B52"	XX
FT	Peptide	154. -162	/note= "Peptide presented by MHC Class I HLA-B52"	DT 31-JUL-2000 (first entry)
FT	Peptide	156. -167	/note= "Peptide presented by MHC Class I HLA-B52"	XX
FT	Peptide	156. -167	/note= "Peptide (AAY52434) presented by MHC Class I HLA-A2"	DE Human tumour antigen, NY-ESO-1 protein.
FT	Peptide	158. -166	/note= "Peptide presented by MHC Class I HLA-A3"	XX
FT	Peptide	159. -167	/note= "Peptide presented by MHC Class I HLA-A3"	XX
FT	Peptide	162. -170	/note= "Peptide presented by MHC Class I HLA-B52"	XX
XX	PN	W09953938-A1.		XX
XX	PD	28-OCT-1999.		XX
XX	PF	24-MAR-1999;	99WO-US006875.	XX
XX	PR	17-APR-1998;	98US-00062422.	XX
XX	PR	02-OCT-1998;	98US-00165546.	XX
XX	PA	(LUDW-) LUDWIG INST CANCER RES.		XX
PI	Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;		PT Tumor-associated antigen useful for cancer immunotherapy is encoded by the open reading frame of LAGE-1 (a tumor-specific antigen) CDNA.	XX
PI	Gure A, Ritter G;		PT the open reading frame of LAGE-1 (a tumor-specific antigen) CDNA.	XX
DR	WPI:2000-038483/03.		PS Example 3; Page 62-63; 73pp; English.	XX
XX	N-PSDB; AA238380.		CC The present sequence is the human NY-ESO-1 protein, a tumour antigen, identified by screening an oesophagus carcinoma cDNA library. This protein is derived from open reading frame (ORF)-1 that contain epitopes of tumour specific T-cells. NY-ESO-1 is expressed in different tumour types, but not in healthy tissues except in testis. It also shows homology with the CAMEL (Cytotoxic T lymphocytes (CTL)-recognised Antigen on Melanoma) protein, a tumour-associated antigen. The tumour-associated antigen displayed on melanoma cells is recognised by cytotoxic T lymphocytes.	CC
XX	PR	98US-00062422.	CC This sequence has anticancer activity. CAMEL tumour antigen and immunogenic peptides derived from it are useful for cancer immunotherapy. They have the potential to induce an immune response, by eliciting a CTL response. The DNA molecule is used for the construction of recombinant or fusion proteins.	CC
XX	PA	02-OCT-1998;	XX	SQ Sequence 180 AA;
XX	PA	98US-00165546.	XX	Query Match 100 %; Score 107; DB 3; Length 180;
XX	XX		Best Local Similarity 100 %; Pred. No. 5.6e-05; Mismatches 0; Indels 0; Gaps 0;	XX
CC	CC	This sequence represents a human tumour antigen, NY-ESO-1, the cDNA encoding which was isolated from an oesophagus squamous cell cancer library. Tissue localisation studies revealed it to be expressed at high levels in normal ovary and testis but not in normal colon, kidney, liver, brain, oesophagus and skin. It was expressed in certain tumours and tumour cell lines with some degree of frequency - these included melanoma specimens and cell lines, and breast and bladder cancer specimens. Expression in other tumour types being sporadic. Peptides derived from NY-ESO-1 are bound by both MHC (major histocompatibility complex) Class I and Class II molecules for presentation to T-cells. Peptides AAY52431- Y52434 bind to Class I HLA-A2 molecules, thereby stimulating T-cell proliferation. The peptides AAY52435-Y52440 bind to Class II HLA-DR53 molecules, stimulating helper T-cell proliferation.	CC	RESULT 7
CC	CC	The peptides derived from NY-ESO-1 may be used in methods and compositions used for the treatment, diagnosis and prevention of cancers (such as melanoma, breast cancer, prostate cancer, lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or lymphoma) and to stimulate the proliferation of T cells.	CC	Qy 1 RGPGRGAAARASPGGGAPR 20
CC	CC	XX	Db 43 RGPGRGAAARASPGGGAPR 62	ID AAB03154 standard; protein; 180 AA.
CC	CC	XX	SQ Sequence 180 AA;	Query Match
CC	CC	XX	100.0%; Score 107; DB 3; Length 180;	

XX AAB03154; XX 23-OCT-2000 (first entry)

XX Human oesophageal cancer-associated antigen NY-ESO-1.

XX oesophageal carcinoma; melanoma; ovary; testis; transmembrane domain; antibody; diagnostic marker; drug delivery target.

XX *Homo sapiens*.

XX

Key Location/Qualifiers

PT Modified-site 7 /note= "Potential N-myristoylation site"

PT Modified-site 9 /note= "Potential N-myristoylation site"

PT Modified-site 11 /note= "Potential O-phosphorylation site"

PT Modified-site 98 /note= "Potential O-phosphorylation site"

PT Modified-site 134 /note= "Potential O-phosphorylation site"

PT Modified-site 138 /note= "Potential O-phosphorylation site"

PT Domain 152..172 /note= "Potential transmembrane domain"

XX US6069233-A.

XX PD 30-MAY-2000.

XX PF 26-JAN-1998; 98US-00013150.

XX PR 03-OCT-1996; 96US-00725181.

XX PA (SLOC) SLOAN KETTERING INST CANCER RES.

XX PA (CORR) CORNELL RES FOUND INC.

XX PA (LUDW) LUDWIG INST CANCER RES.

XX PI Old Lu; Chen Y, Gure AO, Sahin U, Tureci O, PI Freundschuh M;

XX WPI: 2000-410880/35.

XX DR N-PSDS; AAB61483.

XX

PT New isolated esophageal cancer-associated antigen useful as markers for producing antibodies and as targets for identifying abnormal conditions e.g. infections and cancer.

PT Example 5; Fig 3; 9pp; English.

XX This sequence represents a human oesophageal cancer-associated antigen, sequence was isolated from a cDNA library prepared from a specimen of well-to-moderately differentiated squamous cell cancer of the oesophagus. Expression analysis demonstrated that NY-ESO-1 was expressed in oesophageal carcinoma, certain melanoma cell lines and in normal ovary and testis tissue but not in normal colon, kidney, liver or brain tissue. Analysis of the amino acid sequence of the protein indicates that the protein has a transmembrane domain, several N-myristoylation sites and O-phosphorylation sites and that it contains antigenic sequences in the N-terminal half of the protein. The antigen is useful as an immunogen when combined with an adjuvant, in both precursor and post-translationally modified forms, and may be used to generate anti-NY-ESO-1 antibodies. It can also be used as a diagnostic marker for oesophageal cancer, and can be utilised as a marker for the targeted delivery of therapeutic agents to oesophageal cancer cells. It can also be used to generate diagnostic or therapeutic agents.

XX Sequence 180 AA;

XX Query Match 100.0%; Score 107; DB 4; Length 180;

XX Best Local Similarity 100.0%; Pred. No. 5.6e-05;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ID AAB63946 Standard; protein: 180 AA.

XX AC AAB63946;

XX DT 27-APR-2001 (first entry)

XX DE Human NY-ESO-1 protein.

XX KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell; HLA-A2; HLA-DR3; melanoma; adenocarcinoma; bladder carcinoma; non-small cell lung carcinoma; tumour status determination.

XX OS Homo sapiens.

XX PN WO200107917-A1.

XX PD 01-FEB-2001.

XX PP 14-JUL-2000; 2000WO-US019220.

XX PR 23-JUL-1999; 99US-00359503.

XX PA (LUDW) LUDWIG INST CANCER RES.

XX PA (SLOC) SLOAN KETTERING INST CANCER RES.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;

XX DR WPI: 2001-182822/18.

XX DR N-PSDS; AAP58634.

XX PT Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.

XX PT Example 5; Fig 3; 50pp; English.

XX The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a carcinoma, adenocarcinoma, non-small cell lung carcinoma or bladder carcinoma.

XX Sequence 180 AA;

XX Query Match 100.0%; Score 107; DB 4; Length 180;

XX Best Local Similarity 100.0%; Pred. No. 5.6e-05;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX ID AAB63946 Standard; protein: 180 AA.

XX AC AAB63946;

XX DT 27-APR-2001 (first entry)

XX DE Human NY-ESO-1 protein.

XX KW Human; NY-ESO-1; HLA; human leukocyte antigen; CTL; cytotoxic T cell; HLA-A2; HLA-DR3; melanoma; adenocarcinoma; bladder carcinoma; non-small cell lung carcinoma; tumour status determination.

XX OS Homo sapiens.

XX PN WO200107917-A1.

XX PD 01-FEB-2001.

XX PP 14-JUL-2000; 2000WO-US019220.

XX PR 23-JUL-1999; 99US-00359503.

XX PA (LUDW) LUDWIG INST CANCER RES.

XX PA (SLOC) SLOAN KETTERING INST CANCER RES.

XX PA (CORR) CORNELL RES FOUND INC.

XX PI Jager E, Stockert E, Old LJ, Knuth A, Chen Y, Scanlan M;

XX DR WPI: 2001-182822/18.

XX DR N-PSDS; AAP58634.

XX PT Method useful for determining the status (e.g. progression, regression or stability of the disease) of a cancerous condition, involves determining the levels of NY-ESO-1 specific antibodies in a sample taken from a patient.

XX PT Example 5; Fig 3; 50pp; English.

XX The present sequence is human NY-ESO-1 protein. It is provided in a specification relating to a method for determining the status of a cancerous condition in a patient with a tumour that expresses NY-ESO-1. The method comprises assaying a sample taken from the patient for antibodies that specifically bind to the NY-ESO-1 and comparing the value obtained to a prior value obtained from assay of a prior sample taken from the patient. Any difference between the values is indicative of a change in status of the cancerous condition. The method is useful for determining whether a cancerous condition is progressing, regressing or remaining stable, in particular in patients receiving treatment for a carcinoma, adenocarcinoma, non-small cell lung carcinoma or bladder carcinoma.

XX Sequence 180 AA;

XX Query Match 100.0%; Score 107; DB 3; Length 180;

AAG67164
 ID AAG67164 standard; protein; 180 AA.
 XX
 AC AAG67164;
 XX
 DT 13-NOV-2001 (first entry)
 XX
 Amino acid sequence of cancer testis tumour antigen NY-ESO-1.
 DB Cancer testis tumour antigen; NY-ESO-1; LAGE-2; human leukocyte antigen;
 KW HLA; HLA binding peptide; major histocompatibility complex; MHC; tumour;
 KW cancer; testis tumour.
 XX
 OS Homo sapiens.
 XX
 WO200162917-A1.
 PN
 PD 30-AUG-2001.
 XX
 PP 22-JAN-2001; 2001WO-US002126.
 XX
 PR 22-FEB-2000; 2000US-00510635.
 XX
 (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Lethé B., Boon-Faillleur T;
 XX
 DR WPI: 2001-550091/61.
 DR N-PSDB; AA575118.
 XX
 PT Genomic sequences of tumor associated antigen NY-ESO-1 (LAGE-2) useful
 PT for diagnosing testicular tumors.
 XX
 PS Example 5: Fig 3; Sopp; English.
 XX
 CC The present sequence represents cancer testis tumour antigen NY-ESO-1
 * (also called LAGE-2). NY-ESO-1 is a molecule that is processed to at
 CC least one human leukocyte antigen (HLA) binding peptide, which binds to
 CC Class I and Class II major histocompatibility complex (MHC). NY-ESO-1 is
 CC expressed in tumour mRNA and in testis, but not normal colon, kidney,
 CC liver or brain tissue. The presence or level of expression of NY-ESO-1
 CC may be assayed for the diagnosis of cancer, especially testis tumours
 CC Sequence 180 AA;
 CC
 Query Match 100.0%; Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 AC AAU01535;
 XX
 DT 18-JUL-2001 (first entry)
 XX
 DE Human NY-ESO-1 tumour rejection antigen precursor protein.
 KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

FT Modified-site 7 /note= "Myristoylated"
 FT Modified-site 9 /note= "Myristoylated"
 FT Modified-site 11 /note= "Phosphorylated"
 FT Modified-site 98 /note= "Phosphorylated"
 FT Modified-site 134 /note= "Phosphorylated"
 FT Modified-site 138 /note= "Phosphorylated"
 FT Modified-site 200200123560-A2.
 XX
 PN 05-APR-2001.
 XX
 PP 26-SEP-2000; 2000WO-US026411.
 XX
 PR 29-SEP-1999; 99US-00408036.
 XX
 PA (LUDW-) LUDWIG INST CANCER RES.
 XX
 PI Turcic O., Sahin U., Pfreundschuh M;
 XX
 DR WPI; 2001-266156/27.
 XX
 N-PSDB; AA50254.
 PT Polypeptides binding to major histocompatibility complex class II human
 PT leukocyte antigen-determining region molecule having amino acid sequence
 PT found in tumor rejection antigen precursor used for stimulating
 PT proliferation of helper T cells.
 XX
 PS Claim 4; Fig 3; 62pp; English.
 XX
 CC The sequence represents a human NY-ESO-1 tumour rejection antigen
 CC precursor. NY-ESO-1 and SSX-2 polypeptides, or fragments of, bind to
 CC major histocompatibility complex (MHC) Class II molecules such as human
 CC leukocyte antigen-determining region (HLA-DR) molecules and stimulate
 CC proliferation of helper T cells. The peptides can be administered to an
 CC HLA-DR positive subject in order to stimulate the helper T cells. An MHC
 CC Class II HLA-DR/NY-ESO-1/SSX-2 complex expressed on the surface of a cell
 CC or present in free form is useful for this stimulation. The nucleic acid
 CC sequence is useful for screening for a cancerous condition, which involves
 CC contacting a subject sample to a cell line transfected with the
 CC immunoreactive cell (helper T cell), where interaction is indicative of
 CC cancer. In addition, a sample from a patient (for example, a body fluid
 CC or tissue) can be monitored for the amount of the complex present in the
 CC bloodstream. This is useful for determining regression, progression or
 CC onset of a cancerous condition. The method involves contacting the sample
 CC with a radioactive labelled or enzyme labelled monoclonal antibody which
 CC specifically binds with the complex
 XX
 SQ Sequence 180 AA;

Query Match 100.0%; Score 107; DB 4; Length 180;
 Best Local Similarity 100.0%; Pred. No. 5.6e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RGRPGAGARASPGGGGAPR 20
 Db 43 RGRPGAGARASPGGGGAPR 62

RESULT 10
 AAU01535
 ID AAU01535 standard; protein; 180 AA.
 XX
 AC AAU01535;
 XX
 DT 18-JUL-2001 (first entry)
 XX
 DE Human NY-ESO-1 tumour rejection antigen precursor protein.
 KW NY-ESO-1; human; tumour rejection antigen precursor; SSX-2; MHC Class II;
 KW major histocompatibility complex; helper T cell; HLA-DR; cancer;
 KW human leukocyte antigen-determining region; disease progression;
 KW disease regression; disease onset; body tissue; body fluid; enzyme label;
 KW radioactive label; monoclonal antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers

RESULT 11
 AAU07714
 ID AAU07714 standard; protein; 180 AA.
 XX
 AC AAU07714;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human NY ESO-1 protein.

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Search completed: June 22, 2004, 08:51:24
 Job time : 71.6667 secs

Qy 1 RGPRGAGAARASGPGGCAAPR 20
 Db 43 RGPRGAGAARASGPGGCAAPR 62

RESULT 15
 ABR48210
 ID ABR48210 standard; protein; 180 AA.
 XX
 AC ABR48210;
 XX
 DT 12-JUN-2003 (first entry)
 DE Human bladder cancer associated protein sequence SEQ ID NO:139.
 XX
 KW Human; bladder cancer; cytostatic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO2003003906-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 03-JUL-2002; 2002WO-US021338.
 XX
 PR 03-JUL-2001; 2001US-0302814P.
 PR 03-AUG-2001; 2001US-0310099P.
 PR 08-NOV-2001; 2001US-0343705P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 12-APR-2002; 2002US-0372246P.
 XX
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 XX
 PI Mack DH, Aziz N;
 XX
 DR WPI; 2003-201532/9.
 XX
 DR N-PSDB; ACC51024.
 XX
 PT Detecting a bladder cancer-associated transcript in a cell from a patient with a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.
 XX
 PS Claim 10; Page 278; 307pp; English.
 XX
 CC The present invention describes a method for detecting a bladder cancer-
 CC associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridizes to a sequence that is 80 % identical to a
 CC table of sequences (see ACC5091 to ACC51059). ACC5091 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48116 to
 CC ABR48242. Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and
 CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications
 XX
 SQ Sequence 180 AA:
 Query Match 100.0%; Score 107; DB 6; Length 180;
 Best Local Similarity 100.0%; Pred. No 5.6e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGCAAPR 20
 Db 43 RGPRGAGAARASGPGGCAAPR 62

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:49:38 ; Search time 22 Seconds

(without alignments)

46.933 Million cell updates/sec

Title: US-09-529-206D-4_COPY_43_62

Perfect score: 107

Sequence: 1 RGRGAGARASGPGGAPR 20

Scoring table: BLOSUM62

Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

PCST - processing: Minimum Match 0%
 Listing First 45 summaries

Database : Issued Patents AA,*
 1: /cgn2_6/podata/2/aa/5A COMB.pep:
 2: /cgn2_6/podata/2/aa/5B COMB.pep:
 3: /cgn2_6/podata/2/aa/6A COMB.pep:
 4: /cgn2_6/podata/2/aa/6B COMB.pep:
 5: /cgn2_6/podata/2/aa/PC7US COMB.pep:
 6: /cgn2_6/podata/2/aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	107	100.0	180	2	US-08-791-195-9		Sequence 9, Appli
2	107	100.0	180	4	US-09-392-714-25		Sequence 25, Appli
3	101	94.4	180	3	US-08-337-763B-8		Sequence 8, Appli
4	101	94.4	180	4	US-09-751-798-8		Sequence 7, Appli
5	99	92.5	180	2	US-08-191-95-7		Sequence 5, Appli
6	99	92.5	210	2	US-08-191-95-5		Sequence 5, Appli
7	63	58.9	860	4	US-09-252-991A-25681		Sequence 25681, A
8	60	56.1	160	4	US-09-532-991A-27091		Sequence 27091, A
9	60	56.1	928	1	US-08-442-248-2		Sequence 2, Appli
10	60	56.1	928	1	US-08-440-815-2		Sequence 2, Appli
11	60	56.1	928	3	US-08-486-445-2		Sequence 2, Appli
12	60	56.1	928	4	US-08-578-684-2		Sequence 2, Appli
13	60	56.1	1005	2	US-08-469-537A-1-03		Sequence 103, App
14	59	55.1	210	4	US-09-252-991A-24923		Sequence 24923, A
15	59	55.1	330	1	US-08-118-270-21		Sequence 21, Appli
16	59	55.1	330	5	PCT-US3-08128-21		Sequence 21, Appli
17	59	55.1	877	2	US-08-673-789-2		Sequence 2, Appli
18	58	54.2	456	4	US-09-152-991A-17335		Sequence 17335, A
19	58	54.2	700	4	US-09-252-991A-8344		Sequence 28344, A
20	56	52.3	421	4	US-09-252-991A-23235		Sequence 32325, A
21	56	52.3	432	4	US-09-252-991A-23622		Sequence 23622, A
22	55	51.4	191	4	US-09-252-991A-23951		Sequence 23951, A
23	55	51.4	289	4	US-09-252-991A-25496		Sequence 25496, A
24	55	51.4	343	4	US-09-52-991A-23398		Sequence 23398, A
25	54.5	50.9	501	4	US-09-152-991A-32473		Sequence 32473, A
26	54	50.5	140	3	US-09-120-5258-5		Sequence 5, Appli
27	54	50.5	140	4	US-09-347-613C-5		Sequence 5, Appli

Qy	Db	Query Match	Best Local Similarity	Score 107;	DB 2;	Length 180;
		Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
		1 RGRGAGARASGPGGAPR 20				
		43 RGFRGAGARASGPGGAPR 62				

ALIGNMENTS

RESULT 1	US-08-791-495-9	SEQUENCE 9, Application US/08791495
		Patent No. 5811519
		GENERAL INFORMATION:
		APPLICANT: Leth, Bernard
		APPLICANT: Lucas, Sophie
		APPLICANT: De Smet, Charles
		APPLICANT: Godeline, Danièle
		APPLICANT: Boon-Palleur, Thierry
		TITLE OF INVENTION: LI-1 TUMOR SPECIFIC GENES
		NUMBER OF SEQUENCES: 14
		CORRESPONDENCE ADDRESS:
		ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
		STREET: 600 Atlantic Avenue
		CITY: Boston
		STATE: MA
		COUNTRY: USA
		ZIP: 02210
		COMPUTER READABLE FORM:
		COMPUTER: IBM PC compatible
		OPERATING SYSTEM: PC-DOS/MS-DOS
		CURRENT APPLICATION DATA: #1.0, Version #1.25
		APPLICATION NUMBER: US/08/791,495
		FILING DATE:
		CLASSIFICATION: 435
		ATTORNEY/AGENT INFORMATION:
		NAME: Van Amsterdam, John R.
		REGISTRATION NUMBER: 40,212
		REFERENCE/DOCKET NUMBER: L0461/7005
		TELECOMMUNICATION INFORMATION:
		TELEPHONE: 617-720-1500
		TELEFAX: 617-720-2441
		SEQUENCE CHARACTERISTICS:
		LENGTH: 180 amino acids
		TYPE: amino acid
		TOPOLOGY: linear
		MOLECULE TYPE: protein
		US-08-791-495-9

RESULT 2
 US-09-392-714-25
 Sequence 25, Application US/09392714A
 Patent No. 6686147
 GENERAL INFORMATION:
 APPLICANT: Scanlan, Matthew J.
 APPLICANT: Gure, Ali O.
 APPLICANT: Williamson, Barbara
 APPLICANT: Chen, Yao-Tseng
 APPLICANT: Old, Lloyd J.
 TITLE OF INVENTION: Cancer Associated Antigens and Uses
 FILE REFERENCE: L0461/7062
 CURRENT APPLICATION NUMBER: US/09/392,714A
 CURRENT FILING DATE: 1999-09-09
 EARLIER FILING DATE: 1998-07-15
 NUMBER OF SEQ ID NOS: 30
 SEQ ID NO: 25
 LENGTH: 160
 TYPE: PRF
 ORGANISM: Homo sapiens
 US-09-392-714-25

Query Match 100.0% Score 107; DB 4; Length 160;
 Best Local Similarity 100.0%; Pred. No. 2.1e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAASPGGGGAPR 20
 Db 43 RAPRGAGAAASPGGGGAPR 62

RESULT 3
 US-09-937-263B-8
 Sequence 8, Application US/08937263B
 Patent No. 627415
 GENERAL INFORMATION:
 APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
 APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
 APPLICANT: Knuth, Alexander; Old, Lloyd J.;
 TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
 TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
 TITLE OF INVENTION: ITSELF, AND USES THEREOF
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESS: Fullbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/751,798
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/062,422
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/725,182
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 652577man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3158
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180
 TYPE: amino acid
 TOPOLOGY: linear

US-09-937-263B-8

Query Match 94.4% Score 101; DB 4; Length 180;
 Best Local Similarity 95.0%; Pred. No. 9.9e-05;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGPRGAGAAASPGGGGAPR 20
 Db 43 RAPRGAGAAASPGGGGAPR 62

RESULT 5
 US-08-791-495-7
 Sequence 7, Application US/08791495
 Patent No. 5811519
 GENERAL INFORMATION:
 APPLICANT: Leth, Bernard
 APPLICANT: Lucas, Sophie
 APPLICANT: De Smet, Charles
 APPLICANT: Godelaine, Danielle
 APPLICANT: Boon-Falleur, Thierry
 TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/791,495
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Van Amsterdam, John R.
 REGISTRATION NUMBER: 40,212
 REFERENCE/DOCKET NUMBER: 10461/7005
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 617-720-3500
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-791-495-7

Query Match 92.5%; Score 99; DB 2; Length 210;
 Best Local Similarity 95.0%; Pred. No. 0.00019;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAPR 20
 Db 43 RGPRGAGAARASGPGGGAPR 62

RESULT 6
 US-08-791-495-5
 Sequence 5, Application US/08791495
 Patent No. 5811519
 GENERAL INFORMATION:
 APPLICANT: Leth, Bernard
 APPLICANT: Lucas, Sophie
 APPLICANT: De Smet, Charles
 APPLICANT: Godelaine, Danielle
 APPLICANT: Boon-Falleur, Thierry
 TITLE OF INVENTION: LL-1 TUMOR SPECIFIC GENES
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
 STREET: 600 Atlantic Avenue
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

Query Match 92.5%; Score 99; DB 2; Length 180;
 Best Local Similarity 95.0%; Pred. No. 0.00017;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAPR 20
 Db 43 RGPRGAGAARASGPGGGAPR 62

RESULT 7
 US-09-252-991A-25681
 Sequence 23681, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: 1998-02-18
 PRIOR FILING DATE: 1998-02-18
 PRIORITY NUMBER: US 60/074,788
 PRIORITY NUMBER: 107196-136
 FILE REFERENCE: 107196
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO 25681
 LENGTH: 860
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-25681

Query Match 92.5%; Score 99; DB 4; Length 860;
 Best Local Similarity 95.0%; Pred. No. 8.2%;
 Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAP 19
 Db 738 RKGKGSTAAROTSGGGTGP 756

RESULT 8
 US-09-252-991A-27091
 Sequence 27091, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196
 CURRENT APPLICATION NUMBER: US/09/252, 991A
 CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO: 27091
LENGTH: 160

TYPE: PRT
ORGANISM: *Pseudomonas aeruginosa*
US-09-252-991A-27091

Query Match 56.1%; Score 60; DB 4; Length 160;
Best Local Similarity 63.6%; Pred. No. 3.8;
Matches 14; Conservative 0; Mismatches 4; Indels 4; Gaps 1;
Qy 3 PRGAGAARASG---PGGGAPR 20
Db 103 PRGAGAARASGCRCPGPR 124

RESULT 9

US-08-442-248-2

Sequence 2, Application US/08442248

Patent No. 5798448

GENERAL INFORMATION:

APPLICANT: Caras, Ingrid W.
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94090

NUMBER OF SEQUENCES: 18

TITLE OF INVENTION: Al-1 Neurotrophic Factor

CORRESPONDENCE ADDRESS:

APPLICANT: Winslow, John W.
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94090

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/440,815

FILING DATE: 15-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/330128

FILING DATE: 27-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 920C1

REFERENCE DOCKET NUMBER: 920C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 415/952-3881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 928 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-440-815-2

Query Match 56.1%; Score 60; DB 1; Length 928;

Best Local Similarity 61.9%; Pred. No. 19;

Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGAASGPGGG--APR 20

Db 5 GPRGAGRRTQGRGGGDTPR 25

RESULT 11

US-08-486-449-2

Sequence 2, Application US/08486449

Patent No. 6280732

GENERAL INFORMATION:

APPLICANT: Caras, Ingrid W.
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94090

NUMBER OF SEQUENCES: 18

TITLE OF INVENTION: Al-1 Neurotrophic Factor

CORRESPONDENCE ADDRESS:

APPLICANT: Winslow, John W.
ADDRESS: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94090

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/486,449

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/330128

FILING DATE: 27-OCT-1994

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Timothy E.

REGISTRATION NUMBER: 36,700

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-8674

TELEFAX: 415/952-9881

TELEX: 910/371-7168

SEQUENCE CHARACTERISTICS:

LENGTH: 928 amino acids

TYPE: amino acid

TOPOLOGY: linear
US-08-486-449-2

Query Match 56.1%; Score 60; DB 3; Length 928;
Best Local Similarity 61.9%; Pred. No. 19;
Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGSARSGPGGG--APR 20

Db 5 GPRGAGRRTQGRGGGGDTPR 25

RESULT 12

US-08-578-684-2

Sequence 2, Application US/08578684

Patent No. 6610296

GENERAL INFORMATION:

APPLICANT: Caras, Ingrid W.

APPLICANT: Winslow, John W.

TITLE OF INVENTION: AL-1 Neurotrophic Factor

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/578,684

FILING DATE: 02-Jan-1996

CLASSIFICATION: 514

PRIOR APPLICATION:

APPLICATION NUMBER: 08/330128

FILING DATE: 27-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/466449

FILING DATE: 06-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Torchia, Ph.D., Timothy E.

REGISTRATION NUMBER: 36,700

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-8674

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 928 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

US-08-578-684-2

Sequence 1, Application US/08578684

Patent No. 6610296

GENERAL INFORMATION:

Length 928;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

Mismatches 0;

Indels 6;

Gaps 2;

Score 60;

DB 4;

Indels 6;

Gaps 2;

Matches 0;

Conservative 13;

Similarity 56.1%;

Pred. No. 19;

APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196 136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT PUBLISHING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR PUBLISHING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR PUBLISHING DATE: 1998-02-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 4923
 LENGTH: 210
 TYPE: PCT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24923

Query Match 55.1%; Score 59; DB 4; Length 210;
 Best Local Similarity 70.6%; Pred. No. 6.4;
 Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 4 RGAGAAARASGPGGAPR 20
 Db 154 RFACTAAAGGAGGAPR 170

RESULT 15
 US 08-118-270-21
 Sequence 21, Application US/08118270
 Patent No. 550884
 GENERAL INFORMATION
 APPLICANT: Murphy, Randall B.
 APPLICANT: Schusser, David I.
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348

CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROADY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.2.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/118,270
 FILING DATE: 09-SEP-1993

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236
 FILING DATE: 10-SEP-1992

ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.

REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: MURPHY=2A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-727-3528

TELEX: 248633
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 330 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-118-270-21

Query Match 55.1%; Score 59; DB 1; Length 330;
 Best Local Similarity 55.0%; Pred. No. 9.6;

16	99	92.5	180	12	US-10-296-734-834
			17	99	92.5
			18	99	92.5
			19	99	92.5
			20	99	92.5
			21	95	89.8
			22	94	87.9
			23	85	79.4
			24	77	72.0
			25	60	56.1
			26	60	56.1
			27	60	56.1
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מִתְּבָרְכָה מִתְּבָרְכָה מִתְּבָרְכָה מִתְּבָרְכָה מִתְּבָרְכָה מִתְּבָרְכָה

```

FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU FQ7761/00

PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: Patentin version 3.2
SEQ ID NO: 832
LENGTH: 180
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: NYNSOLA consensus polypeptide
US-10-296-734-832

Query Match 100.0%; Score 107; DB 12; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Query Match 100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

RESULT 5
US-10-117-937-74
Sequence 74, Application US/10117937
Publication No. US20030220239A1
GENERAL INFORMATION:
APPLICANT: CTL IMMUNOTHERAPIES CORP.
SIMARD, John, J.L.
DIAMOND, David, C.
LIU, Liping
XIE, Zhidong
TITLE OF INVENTION: EPITOPE SEQUENCES
FILE REFERENCE: C1LMM-027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FastSBQ for Windows Version 4.0
SEQ ID NO: 74
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-117-937-74

Query Match 100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0; Query Match 100.0%; Score 107; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;
Matches 20; Conservative 0; Mismatches 0;

RESULT 6
US-10-295-027-386
Sequence 386, Application US/10295027
Publication No. US2003023230A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
AZIZ, Natasha
Ginsberg, Wendy M.
Gish, Kurt C.
Glynn, Richard
Hevez, Peter A.
Mack, David K.
Murray, Richard
Watson, Susan R.
Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
Methods of Screening for Modulators of Cancer
FILE REFERENCE: C1LMM-21CP1C
CURRENT APPLICATION NUMBER: US/10/026,066
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 09/561,074
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 09/560,465
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 09/561,572
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 09/561,571
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: PCT/US01/13806
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US

```

CURRENT APPLICATION NUMBER: US/10/295,027
 CURRENT FILING DATE: 2002-11-13
 PRIOR APPLICATION NUMBER: US 09/663,733
 PRIOR FILING DATE: 2000-09-15
 PRIOR APPLICATION NUMBER: US 60/350,666
 PRIOR APPLICATION NUMBER: US 60/335,394
 PRIOR FILING DATE: 2001-11-13
 PRIOR APPLICATION NUMBER: US 60/332,464
 PRIOR APPLICATION NUMBER: US 60/334,393
 PRIOR FILING DATE: 2001-11-19
 PRIOR APPLICATION NUMBER: US 60/340,376
 PRIOR FILING DATE: 2001-12-14
 PRIOR APPLICATION NUMBER: US 60/347,211
 PRIOR FILING DATE: 2002-01-08
 PRIOR APPLICATION NUMBER: US 60/347,349
 PRIOR FILING DATE: 2002-01-10
 PRIOR APPLICATION NUMBER: US 60/355,250
 PRIOR FILING DATE: 2002-02-08
 PRIOR APPLICATION NUMBER: US 60/356,714
 PRIOR FILING DATE: 2002-02-13
 Remaining Prior Application data removed - See File Wrapper or PAlM.
 NUMBER OF SEQ ID NOS: 1386
 SEQ ID NO: 386
 SOFTWARE: Patentin Ver. 2.1
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-295-027-386

Query Match 100.0%; Score 107; DB 15; Length 180;
 - Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

Qy 1 RGPRGAAARASGPGGGAPR 20
 Db 43 RGPRGAAARASGPGGGAPR 62

RESULT 7
 US-10-188-832-139

Sequence 139, Application US/10/88832
 Publication No. US20040076955A1
 GENERAL INFORMATION:
 APPLICANT: Mack, David H.
 APPLICANT: Aziz, Natascha
 APPLICANT: Bos Biotechnology, Inc.
 TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer. Compositions and Methods of Screening for Modulators of Bladder Cancer
 FILE REFERENCE: 018501-002330US
 CURRENT FILING DATE: 2002-11-22
 PRIOR FILING DATE: 2001-07-03
 PRIOR APPLICATION NUMBER: US 60/302,814
 PRIOR FILING DATE: 2001-08-03
 PRIOR APPLICATION NUMBER: US 60/310,099
 PRIOR FILING DATE: 2001-11-08
 PRIOR APPLICATION NUMBER: US 60/343,705
 PRIOR FILING DATE: 2002-04-12
 NUMBER OF SEQ ID NOS: 207
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 139
 LENGTH: 180
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-188-832-139

Query Match 100.0%; Score 107; DB 16; Length 180;

Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;

Qy 1 GPRGAAARASGPGGGAPR 19
 Db 43 GPRGAAARASGPGGGAPR 19

RESULT 8
 US-09-821-883-27

Sequence 27, Application US/09821883
 Patent No. US2002061310A1
 GENERAL INFORMATION:
 APPLICANT: Laus, Reiner
 APPLICANT: Vidovic, Damir
 APPLICANT: Groddis, Thomas
 TITLE OF INVENTION: Compositions and Methods for Dendritic Cell-Based Immunotherapy
 FILE REFERENCE: 7635-0022,300
 CURRENT APPLICATION NUMBER: US/09/821,883
 CURRENT FILING DATE: 2001-03-30
 PRIOR APPLICATION NUMBER: US 60/193,504
 PRIOR FILING DATE: 2000-03-30
 NUMBER OF SEQ ID NOS: 30
 SEQ ID NO: 27
 LENGTH: 397
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: NY-ESO-1C tumor antigen
 US-09-821-883-27

Query Match 100.0%; Score 107; DB 9; Length 397;
 - Best Local Similarity 100.0%; Pred. No. 0.00065; Indels 0; Gaps 0;
 Matches 20; Conservative 0; Mismatches 0;

Qy 1 RGPRGAAARASGPGGGAPR 20
 Db 43 RGPRGAAARASGPGGGAPR 62

RESULT 9
 US-10-296-734-1404

Sequence 1404, Application US/10296734
 Publication No. US20040054137A1
 GENERAL INFORMATION:
 APPLICANT: Thompson, Scott A
 APPLICANT: Ranshaw, Ian A
 TITLE OF INVENTION: Synthetic molecules and uses therefor
 FILE REFERENCE: Savine
 CURRENT FILING DATE: 2003-08-04
 PRIOR APPLICATION NUMBER: AU PQ7761/00
 PRIOR FILING DATE: 2000-05-26
 NUMBER OF SEQ ID NOS: 1507
 SOFTWARE: Patentin version 3.2
 SEQ ID NO: 1404
 LENGTH: 30
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: NYS01a segment 4
 US-10-296-734-1404

Query Match 95.3%; Score 102; DB 12; Length 30;
 - Best Local Similarity 100.0%; Pred. No. 0.00033; Indels 0; Gaps 0;

Qy 2 GPRGAAARASGPGGGAPR 20
 Db 1 GPRGAAARASGPGGGAPR 19

Query Match 100.0%; Score 107; DB 16; Length 180;

RESULT 10
 US-10-296-734-1454
 Sequence 1454, Application US/10296734
 GENERAL INFORMATION:
 APPLICANT: Thompson, Scott A
 APPLICANT: Ramshaw, Ian A
 TITLE OF INVENTION: Synthetic molecules and uses therefor
 FILE REFERENCE: Savine
 CURRENT APPLICATION NUMBER: US/10/296,734
 PRIOR APPLICATION NUMBER: AU PQ7761/00
 PRIOR FILING DATE: 2003-08-04
 NUMBER OF SEQ ID NOS: 1507
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 1454
 LENGTH: 3541
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: Melanoma cancer specific Savine

Query Match 95.2%; Score 102; DB 12; Length 3541;
 Best Local Similarity 100.0%; Pred. No. 0.015; Indels 0; Gaps 0;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GPRGAGARASPGGGAPR 20
 Db 23539 GPRGAGARASPGGGAPR 2377

RESULT 11
 US-09-751-798-8
 Sequence 8, Application US/09751798
 Patent No. US20020010321A1

GENERAL INFORMATION:
 APPLICANT: Stockert, Elisabeth; Jager, Elke;
 APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
 APPLICANT: Knuth, Alexander; Old, Lloyd J.
 TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
 TITLE OF INVENTION: Associated Proteins, Uses Thereof,
 NUMBER OF SEQUENCES: 8
 TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Fulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/023,182
 FILING DATE: 17-Dec-2001
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/10/023,182
 FILING DATE: 17-Dec-2001
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. US20020164665Alman D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466 .3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3168
 TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 180
 TYPE: amino acid
 TOPOLOGY: linear

US-10-023-182-8

RESULT 12
 US-10-023-182-8
 Sequence 8, Application US/10023182
 Publication No. US20020164665A1
 GENERAL INFORMATION:
 APPLICANT: Stockert, Elisabeth; Jager, Elke;
 APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
 APPLICANT: Knuth, Alexander; Old, Lloyd J.
 TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
 TITLE OF INVENTION: Associated Proteins, Uses Thereof,
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSSEE: Fulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue
 CITY: New York City
 STATE: New York
 COUNTRY: USA
 ZIP: 10103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/023,182
 FILING DATE: 17-Dec-2001
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/10/023,182
 FILING DATE: 17-Dec-2001
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. US20020164665Alman D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466 .3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3168
 TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Qy 1 RGRGAGARASPGGGAPR 20
 Db 43 RAPRGAGARASPGGGAPR 62

RESULT 13
 US-10-023-182-8

Db 43 RAPRGAGAARASGPGGGAPR 62

; PRIOR APPLICATION NUMBER: US 60/356,714

RESULT 13
US-10-364-614-14
Sequence 14, Application US/10364614
Publication No. US2003017520A1
GENERAL INFORMATION:
APPLICANT: JAGER, Elke
APPLICANT: KNUTH, Alexander
APPLICANT: OLD, Lloyd
APPLICANT: Gnjalic, SachaFILE REFERENCE: IUD 5126.1 CIP 14
TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/364,614
CURRENT FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 60/355,828
PRIOR FILING DATE: 2002-02-13
NUMBER OF SEQ ID NOS: 17SOFTWARE: PatentIn version 3.2
SEQ ID NO 14
LENGTH: 180
TYPE: PRT
ORGANISM: Homo sapiens
US-10-364-614-14Query Match 94.4%; Score 101; DB 14; Length 180;
Best Local Similarity 95.0%; Pred. No. 0.0014;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RAPRGAGAARASGPGGGAPR 20
Db 43 RAPRGAGAARASGPGGGAPR 62RESULT 14
US-10-295-027-388
Sequence 388, Application US/10295027
Publication No. US20030323350A1
GENERAL INFORMATION:
APPLICANT: Arar, Daniel
APPLICANT: Ariz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Gish, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezsi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosing of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US 60/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 60/363,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393.
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08

; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 388
; LENGTH: 135
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-388

Query Match 92.5%; Score 99; DB 15; Length 135;
Best Local Similarity 95.0%; Pred. No. 0.0018;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 RGPRGAGAARASGPGGGAPR 20
Db 43 RGPRGAGAARASGPGGGAPR 62

RESULT 15
US-10-188-832-141
Sequence 141, Application US/10188832
Publication No. US20040076955A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Eos Biotechnology, Inc.
APPLICANT: Mack, David H.
APPLICANT: Ariz, Natasha
TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions and Methods of Screening for Modulators of Bladder
TITLE OF INVENTION: Cancer
FILE REFERENCE: 018501-0023300S
CURRENT APPLICATION NUMBER: US/10/188,832
CURRENT FILING DATE: 2002-11-22
PRIOR APPLICATION NUMBER: US 60/302,814
PRIOR FILING DATE: 2001-07-03
PRIOR APPLICATION NUMBER: US 60/310,099
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/343,705
PRIOR FILING DATE: 2001-11-08
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/372,246
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 207
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 141
LENGTH: 135
TYPE: PRT
ORGANISM: Homo sapiens
US-10-188-832-141

Query Match 92.5%; Score 99; DB 16; Length 135;
Best Local Similarity 95.0%; Pred. No. 0.0018;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 RGPRGAGAARASGPGGGAPR 20
Db 43 RGPRGAGAARASGPGGGAPR 62

Search completed: June 22, 2004, 08:56:18
Job time : 52 secs

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OM protein - protein search, using sw model

Run on: June 22, 2004, 08:48:03 ; Search time 18 Seconds
 (without alignments)

106.879 Million cell updates/sec

Title: US-09-529-206D-4_COPY_43_62

Perfect score: 107

Sequence: 1 RGPRGAGARASGPGGGAFR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : PIR_78:*

1: PIR:*

2: PIR:*

3: PIR:*

4: PIR:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	67	62.6	627	2	T35608	polyketide hydroxylase - Streptomyces coelicolor
2	60	56.1	893	2	S51603	C;Species: Streptomyces coelicolor
3	60	56.1	981	2	S51604	C;Accession: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Mar-2000
4	60	56.1	1005	2	S49015	R;Seeger, K.J.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
5	59	55.1	129	1	OTRSB	submitted to the EMBL Data Library, June 1999
6	59	55.1	877	2	149867	A;Reference number: Z21584
7	58.5	54.7	566	2	T21096	A;Accession: T35608
8	58.5	54.7	692	2	T21095	A;Molecule type: DNA
9	57	53.3	129	1	JC2254	A;Cross-references: EMBL:AL079356; PIDN:CAB45603_1; GSPDB:GN00070; SCGDB:SC6G9_12C
10	57	53.3	355	2	T36273	C;Genetics:
11	56	52.3	331	2	S78432	C;Superfamily: tetracycline 6-hydroxylase
12	55	51.4	201	2	C40040	Query Match 62.6%; Score 67; DB 2; Length 627;
13	55	51.4	201	2	S26404	Best Local Similarity 75.0%; Pred. No. 2; Mismatches 0; Indels 0; Gaps 0;
14	55	51.4	248	2	A40040	Qy 2 GPRGAGAARASGPGGG 17
15	55	51.4	250	2	T46417	Db 447 GPRGAGAAGGGPGGG 462
16	55	51.4	292	2	B40040	RESULT 2
17	54	51.4	1215	2	T32234	polyketide hydroxylase - rat
18	54	50.9	495	2	F83124	receptor-like tyrosine kinase Btk-1 - rat
19	54	50.5	388	2	T29173	C;Species: Rattus norvegicus (Norway rat)
20	54	50.5	597	2	S51212	C;Accession: 07-May-1995 #sequence_revision 21-Jul-1995
21	54	50.5	730	2	A36226	R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
22	54	50.5	1733	2	B45244	Oncogene 3, 3277-3288, 1993
23	53	50.0	627	2	A44112	A;Title: Btk-1 and Btk-2: two novel members of the Eph receptor-like tyrosine kinase family
24	53	50.0	3190	2	T13838	A;Reference number: S49015; PMID:94067777; PMID:7504232
25	53	49.5	485	1	F71235	A;Accession: S51603
26	53	49.5	1306	2	A70934	A;Molecule type: mRNA
27	52.5	49.1	450	2	A40169	A;Cross-references: EMBL:S68028
28	52.5	49.1	782	2	S33945	A;Note: the authors translated the codon GAC for residue 170 as Glu
29	52.5	49.1	1690	2	T356394	C;Superfamily: protein kinase homology <KIN>

ALIGNMENTS

MEGFS protein - hu	30	52.5	49.1	1737	2	T00209
Probable ring finger protein - homobox protein H	31	52	48.6	295	2	T04483
homeobox protein H	32	52	48.6	314	2	JC5273
immediate-early protein	33	52	48.6	373	2	A47234
immediate-early protein	34	52	48.6	676	1	BDBE22
probable quinolinate	35	52	48.6	676	1	BDBE23
brain specific angiotensin receptor-like receptor	36	52	48.6	1171	2	T42372
immediate-early protein	37	52	48.6	1256	2	JE0209
155K transcription factor	38	52	48.6	1487	1	3DBEB1
hypothetical protein	39	52	48.6	1487	1	EDBEF6
transcription factor	40	51.5	48.1	1958	2	B40505
fibrillarin [importin	41	51	47.7	198	2	A57717
octamer binding transcription factor	42	51	47.7	327	2	T47231
collagen alpha 1 C	43	51	47.7	420	2	I59234
probable ATP-dependent	44	51	47.7	632	2	S42731
	45	51	47.7	688	2	T48796

Qy 2 GPRGAGAARASGPGGG--APR 20
 Db 5 GPRGAGRRTQGRGGGDTPR 25

RESULT 3
 S51604 receptor-like tyrosine kinase Bhk-1 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: S51604
 C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
 R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
 Oncogene 8, 3277-3288, 1993
 A;Title: Bhk-1 and Bhk-2: two novel members of the Eph receptor-like tyrosine kinase fam
 A;Reference number: S49015; MUID:94067777; PMID:7504232
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-981 <MAI>
 A;Cross-references: EMBL:S68029

C;Note: the authors translated the codon GAC for residue 170 as Glu
 C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C;Keywords: APB; transmembrane protein
 F;651-917;Domain: protein kinase ATP-binding motif

Query Match Score 60; DB 2; Length 981;
 Best Local Similarity 61.9%; Pred. No. 17;
 Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGAARASGPGGG--APR 20
 Db 5 GPRGAGRRTQGRGGGDTPR 25

RESULT 4
 S49015 receptor-like tyrosine kinase Bhk-1 - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Accession: S49015; S51602
 R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
 Oncogene 8, 3277-3288, 1993
 A;Title: Bhk-1 and Bhk-2: two novel members of the Eph receptor-like tyrosine kinase fam
 A;Reference number: S49015; MUID:94067777; PMID:7504232
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-1005 <MAI>
 A;Cross-references: EMBL:S68024

C;Note: the authors translated the codon GAC for residue 170 as Glu
 C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 C;Keywords: APB; transmembrane protein
 F;675-941;Domain: protein kinase ATP-binding motif

Query Match Score 60; DB 2; Length 1005;
 Best Local Similarity 61.9%; Pred. No. 18;
 Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

RESULT 5

ORTHUSB
 cytochrome-c oxidase (EC 1.9.3.1) chain Vb precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Mar-1992 #sequence_revision 07-Jun-1996 #text_change 11-Jun-1999
 C;Accession: JT0324; A39063; S7198; A39817
 R;Zeviani, M.; Sakoda, S.; Sherbony, A.A.; Nakase, H.; Rizzuto, R.; Samitt, C.E.; DiMat
 Gene 65, 1-11, 1988
 A;Title: Sequence of cDNAs encoding subunit Vb of human and bovine cytochrome c oxidase
 A;Reference number: JT0324; MUID:8284368; PMID:2840351
 A;Accession: JT0324
 A;Molecule type: mRNA
 A;Residues: 1-129 <ZEV>
 A;Cross-references: EMBL:M19961; NID:9180940; PIDN:AAA52061.1; PID:9180941
 R;Lomax, M.I.; Hsieh, C.L.; Darras, B.T.; Francke, U.
 Genomics 10, 1-9, 1991
 A;Title: Structure of the human cytochrome c oxidase subunit Vb gene and chromosomal m
 A;Reference number: A39063; MUID:91257815; PMID:1646156
 A;Accession: A39063
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-108 'E' 110-129 <LOM>
 A;Cross-references: EMBL:M59250
 A;Note: the authors translated the codon GGC for residue 21 as His
 R;Bachman, N.J.; Yang, T.L.; Dosen, J.S.; Ernst, R.E.; Lomax, M.I.
 Arch. Biochem. Biophys. 333, 152-162, 1996
 A;Title: Phylogenetic footprinting of the human cytochrome c oxidase subunit Vb promoter
 A;Reference number: S74198; MUID:96400390; PMID:8806766
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-35, 'TR' <BAC>
 A;Cross-references: EMBL:U41284; PID:91679627; PIDN:AA819185.1; PID:91679628
 C;Genetics:
 A;Gene: GDB:COX5B
 A;Cross-references: GDB:127530; OMIM:123866
 A;Map Position: 2cen-2q13
 A;Genome: nuclear
 C;Complex: Part of a 13 chain complex spanning the inner mitochondrial membrane and cor
 (see PIR:OMHUSA), Vb, via (see PIR:OGH62), Vb (see PIR:OGH62), Vb (see PIR:OGH62C)
 m dimers within the mitochondrial inner-membrane
 C;Function:
 A;Description: the cytochrome-c oxidase complex catalyzes the oxidation of four molecu
 lns from the mitochondrial matrix producing two molecules of water and lowering the conc
 A;Note: the role of chain Vb is not clear
 C;Superfamily: mammalian cytochrome-c-oxidase chain Vb
 C;Keywords: electron transfer; membrane-associated complex; mitochondrial inner membr
 F;1-31;Domain: transit peptide (mitochondrion); status predicted <TPN>
 F;32-129;Product: cytochrome-c oxidase chain Vb #status predicted <TPN>
 F;91-93;113-116;Binding site: zinc (Cys) #status predicted <TPN>
 Query Match Score 55.1%; Pred. No. 4.5%;
 Best Local Similarity 57.9%; Mismatches 7; Indels 0; Gaps 0;
 Matches 11; Conservative 1;
 Qy 1 RGPRQAGARASGPGGAP 19
 Db 20 RGPGGAAAMRSWASGG3VP 38

RESULT 6
 I48967
 brain-specific kinase - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
 C;Accession: I48967
 R;Zhou, R.R.; Copeland, T.D.; Kromer, L.F.; Schulz, N.T.
 J. Neurosci. Res. 37, 129-143, 1994
 A;Title: Isolation and characterization of Bsk, a growth factor receptor-like tyrosine
 A;Reference number: I48967
 A;Accession: I48967
 A;Status: preliminary; translated from GB/EMBL/DB/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-877 <RES>

A; Cross-references: EMBL:U07357; PIDN:9466369; PIDN:AA17038.1; PID:9466370
 C; Genetics:
 C; Species: Bsk

C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat
 F; Best Local Similarity 55.1%; Score 59; DB 2; Length 877;
 Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
 Qy 2 GPGAGAARASGGGG- APR 20
 Db 5 GPGAGAATRGGGGDTPR 25

A; Cross-references: EMBL:Z501010; PIDN:CAA90444.1; GSPDB:GN00028; CESP:F18H3.3a
 C; Genetics:
 C; Species: Caenorhabditis elegans

C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C; Accession: T21096
 R; Coles, L.
 A; Reference number: Z19373
 A; Accession: T21096
 A; Status: Preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-566 <WIL>
 A; Cross-references: EMBL:Z501010; PIDN:CAA90444.1; GSPDB:GN00028; CESP:F18H3.3b
 A; Experimental source: Clone F18H3
 C; Genetics:
 A; Gene: CESP:F18H3.3b
 A; Map position: X
 A; Introns: 111/1; 215/2; 469/3; 552/3
 C; Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
 Query Match 54.7%; Score 58.5; DB 2; Length 566;
 Best Local Similarity 65.0%; Pred. No. 16;
 Matches 13; Conservative 0; Mismatches 4; Indels 3; Gaps 1;
 Qy 3 PRGAGAARASGGPG--GGP 19
 Db 530 PRDAGAPRGGGGPVGQMGCGAP 549

RESULT 8
 T21095
 hypothetical protein F18H3.3a - Caenorhabditis elegans
 C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
 C; Accession: T21095
 R; Coles, L.
 A; Reference number: Z19373
 A; Accession: T21095
 A; Status: Preliminary; translated from GB/EMBL/DDBJ
 A; Molecule type: DNA
 A; Residues: 1-692 <WIL>
 A; Cross-references: EMBL:Z501010; PIDN:CAA90444.1; GSPDB:GN00028; CESP:F18H3.3a
 C; Genetics:
 A; Gene: CESP:F18H3.3a
 A; Map position: X
 A; Introns: 111/1; 215/2; 469/3; 552/3
 C; Superfamily: polyadenylate-binding protein; ribonucleoprotein repeat homology
 Query Match 54.7%; Score 58.5; DB 2; Length 692;
 Best Local Similarity 65.0%; Pred. No. 19;
 Matches 13; Conservative 0; Mismatches 4; Indels 3; Gaps 1;

Qy 3 PRGAGAARASGGPG--GGP 19
 Db 530 PRDAGAPRGGGGPVGQMGCGAP 549

RESULT 9
 JC2254
 cytochrome-c oxidase (EC 1.9.3.1) chain Vb precursor - rat

N; Alternative names: cytochrome-c oxidase (EC 1.9.3.1) chain Vta*
 C; Species: Ratmus norvegicus (Norway rat)

C; Date: 28-Oct-1994 #sequence_revision 26-May-1995 #text_change 16-Jun-2000

C; Accession: JC2254; S0255; S63375

R; Hoshinaga, H.; Amuro, N.; Goto, Y.; Okazaki, T.
 J. Biochem. 115: 194-201, 1994

A; Title: Molecular cloning and characterization of the rat cytochrome c oxidase subunit

A; Reference number: JC2254; MUID:94266742; PMID:8206867

A; Accession: JC2254

A; Molecule type: mRNA
 A; Residues: 1-129 <ROS>

A; Cross-references: DDBJ:D10952; NID:9193694; PIDN:BAK01744.1; PID:9193695

A; Experimental source: liver

A; Accession: JC2255

A; Molecule type: DNA
 A; Residues: 1-129 <FO2>

A; Cross-references: DDBJ:D10951

A; Molecule type: mRNA
 A; Residues: 1-129 <HO2>

A; Cross-references: EMBL:X142008

A; Species: Lambda COXIVb741

R; Goto, Y.; Okazaki, T.

Nucleic Acids Res. 17: 6388, 1989

A; Title: Cytochrome-c oxidase sequence of cDNA for rat liver and brain cytochrome c oxidase subunit

A; Reference number: S05318; MUID:89366668; PMID:2549512

A; Accession: S05318

A; Molecule type: mRNA
 A; Residues: 31-129 <GOT>

A; Cross-references: EMBL:X142008

A; Species: Ratmus norvegicus (Norway rat)

R; Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jagow, G.

Biochim. Biophys. Acta 235-241, 1995

A; Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-acid

A; Reference number: S65372; MUID:95324529; PMID:7601105

A; Accession: S65375

A; Molecule type: protein
 A; Residues: 32-41 <SCH>

A; Experimental source: liver

C; Genetics:

A; Gene: COXIVb-1

A; Introns: 35/1; 59/3; 93/1

A; Note: intronless gene COXIVb-2 apparently a nonfunctional processed pseudogene

C; Superfamily: mammalian cytochrome-c oxidase chain Vb

C; Keywords: membrane-associated complex; mitochondrial inner membrane; mitochondrion

P; 1-31/Domain: transit peptide (mitochondrion) #status predicted <NAT>

P; 32-129/Product: cytochrome-c oxidase chain Vb #status predicted <NAT>

Query Match 53.3%; Score 57; DB 1; Length 129;

Best Local Similarity 55.6%; Pred. No. 74;

Matches 10; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Cy 2 GPRGAGAARASGGCCGAP 19

Db 21 GPRGAGAATRSMASGGCVP 38

RESULT 10
 T36273

hypothetical protein SCR68-23c - Streptomyces coelicolor

C; Species: Streptomyces coelicolor

C; Date: 01-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jun-2000

C; Accession: T36273

R; Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, June 1999

A; Reference number: 221576

A; Accession: T36273

A; Status: preliminary; translated from GB/EMBL/DBSJ

A; Molecule type: DNA

A; Residues: 1-355 <MUR>

A;Cross-references: EMBL:AU039345; PIDN:CAP45359.1; GSPDB:GN00070; SCOEDB:SCB68.23C
 A;Experimental source: strain A3 (2)
 C;Genetics:
 A;Gene: SCOEDB:SCB68.23C
 C;Superfamily: Streptococci coelicolor hypothetical protein SCB68.23C

Query Match 53.3%; Score 57; DB 2; Length 355;
 Best Local Similarity 57.9%; Pred. No. 17; Indels 0; Gaps 0;
 Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
 Query 1 RGPRGAGAAARASGPGGAP 19
 Db 15 RSGRGAGGRRGGPAAESAP 33

RESULT 11
 S78452
 POU-domain protein rdc-1 - human
 C;Species: Homo sapiens (man)
 C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 24-Sep-1999
 C;Cross-references: EMBL:X64624; NID:G35914; PIDN:CAA45907.1; PID:G35915
 C;Accession: S78452; S26063; T38151
 R;Alt., F.W.
 R;Title: A novel POU homeodomain gene specifically expressed in cells of the developing
 A;Reference number: S78452
 A;Accession: S78452
 A;Residues: 174-177,'S',179-233,'K',235-327 <COL>
 A;Cross-references: EMBL:X64624
 A;Experimental source: placenta
 C;Superfamily: unassigned homeobox proteins; homeobox homeoCPY; POU domain homology
 C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
 F;181-250/Domain: POU domain homology <POU>
 F;181-324/Domain: homeobox homology <HOX>

Query Match 52.3%; Score 56; DB 2; Length 331;
 Best Local Similarity 61.1%; Pred. No. 20; Indels 3; Gaps 1;
 Matches 11; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

Query 2 GPRGAGAAARASGPGGAP 19
 Db 65 GPRGGG---GGPGGGP 78

RESULT 12
 C40040
 alternative splicing factor ASF-3 - human
 C;Species: Homo sapiens (man)
 C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #text_change 03-Dec-1999
 C;Cross-references: C40040
 R;Ge, H.; Zuo, P.; Manley, J.L.
 Cell 66, 373-382, 1991
 A;Title: Primary structure of the human splicing factor ASF reveals similarities with Dr
 A;Reference number: A40040; MUID:91309149; PMID:1855257
 A;Accession: C40040
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-248 <GR>
 R;Krainer, A.R.; Mayeda, A.; Rozak, D.; Birnstiel, M.
 Cell 66, 383-394, 1991
 A;Title: Functional expression of cloned human splicing factor SF2: homology to RNA-BP
 A;Accession: B40041
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-248 <RPA>
 A;Cross-references: GB:MT2709; NID:9179073; PIDN:AAA35565.1; PMID:9179075
 R;Ge, H.; Zuo, P.; Manley, J.L.
 Cell 66, 383-394, 1991
 A;Title: Functional expression of cloned human splicing factor SF2: homology to RNA-BP
 A;Accession: B40041
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-248 <RPA>
 A;Cross-references: GB:MT2709; NID:9179073; PIDN:AAA35565.1; PMID:9179075
 C;Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoproteins
 F;17-81/Domain: ribonucleoprotein repeat homology <RPA1>
 F;17-81/Domain: ribonucleoprotein repeat homology <RPA2>

Query Match 51.4%; Score 55; DB 2; Length 201;
 Best Local Similarity 55.0%; Pred. No. 18; Indels 0; Gaps 0;
 Matches 11; Conservative 0; Mismatches 0; Indels 9; Gaps 0;

RESULT 15

PT DOMAIN 5 82 GLY-RICH.
 PT TRANSMEM 156 172 POTENTIAL MW: B122C5C28BR1569 CRC64;
 SQ SEQUENCE 180 AA; 17992 MN; B122C5C28BR1569 CRC64;
 Query Match 100.0%; Score 107; DB 1; Length 180;
 Best Local Similarity 100.0%; Pred. No. 2-De-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RGPRGAGAARASGPCCGAPR 20
 Db 43 RGPRGAGAARASGPCCGAPR 62

RESULT 2
 CRG2_HUMAN STANDARD; PRT; 210 AA.
 ID CTG2_HUMAN STANDARD; PRT; 210 AA.
 AC 075638; 075637; 39, Created
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cancer/testis antigen 2 (LAGE-1 protein).
 DE CTAG2 OR LAGE1.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
 OX NCBI TaxID:9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3 (2) / M145;
 RX MEDLINE=21986410; PubMed=12000953;
 RA Bentley S.D., Chater K.P., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabbinkowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hedges D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3 (2)." [2]
 RN [2]
 RP SEQUENCE OF 1-255 FROM N.A.
 RC STRAIN-A3 (2);
 RX MEDLINE=94075247; PubMed=8253693;
 RA Blanco G., Pereda A., Brian P., Mendez C., Chater K.F., Salas J.A.;
 RT "A hydroxylase-like gene product contributes to synthesis of a
 polyketide spore pigment in Streptomyces halstedii." [3]
 PT polyketide
 RL J-Bacteriol. 175:8043-8048 (1993).
 CC -!- FUNCTION: Involved in developmentally regulated synthesis of a
 CC compound biosynthetically related to polyketide antibiotics which
 CC is essential for spore color in Streptococcus coelicolor.
 CC -!- COFACTOR: FAD (By similarity).
 CC -!- SIMILARITY: BELONGS TO THE PHEA/TFDB FAMILY OF FAD MONOOXYGENASES.
 CC -----
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 CC -----
 DR EMBL; AJ233093; CRA1117.1;
 DR EMBL; AJ233040; CAA11043.1;
 DR EMBL; AJ233041; CAA11044.1;
 DR Genew; HGNC:2442; CTAG2.
 DR MIM: 300396; -
 KW Polymorphism; Alternative splicing; Transmembrane; Antigen.
 PT DOMAIN 5 79 GLY-RICH.
 PT DOMAIN 183 188 POLY-PRO.
 PT VARSPLIC 135 210 MSWDDPREGAGRMVYVGIGLGSASPEGQKARDLRTPKKV
 PT SQRPTPQGPQPGQGQDGRGVAFNVEFSAPI -> IR
 PT LTAADERQLOQISSLQQLSLMMTTCPLPVFLAQASG
 PT ORR (in isoform LAGE-1A). /FTid-VP_004301.
 PT VARIANT 6 6 R -> Q.
 PT VARIANT 89 89 E -> Q. /FTid-VP_007855.
 PT VARIANT 5 79 E -> Q. /FTid-VP_007856.

PRINTS: PR00420; RINGNOXGNASE.
 Oxidoreductase; Flavoprotein; PAD; Complete proteome.
 XW 22 FAD (POTENTIAL).
 NP BIND 51 FAD (POTENTIAL).
 NP BIND 309 319 R -> A (IN REF 2).
 FT 60 60 L -> LH (IN REF 2).
 CONFLICT 145 145 C -> S (IN REF 2).
 CONFLICT 234 234 S (IN REF 2).
 SEQUENCE 627 AA; 64557 MW; 74688AA2A9E951IC CRC64;
 Query Match: 62.6%; Score: 67; DB 1; Length: 627;
 Best Local Similarity: 75.0%; Pred. No. 1.7;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Qy 2 GPRGAGA|RASGPGGG 17
 Db 447 GPRGAGGAGGGPGGG 462
 SEQUENCE 337 AA: 36714 MW; EC8B4A1414756CB CRC64;

RESULT 4
 CT86_HUMAN STANDARD PRT; 337 AA.
 AC Q9BZ19;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Hypothetical protein c20orf86.
 GN C20QRF86.
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;
 Mammalia; Eutheria; Primates; Catarrini; Homiridae; Homo.
 OX NCBI_TaxID=9606;
 RN [1] _
 SEQUENCE FROM N.A.
 - RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J.J., Burton J., Gilbert J.G.R.,
 Jones M., Stavridis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Beard L.M., Barlow K.P., Bates N., Bird C.P., Blakey S.B., Babbage A.K., Bagguley C.L.,
 RA Beasley O.P., Bird A.P., Blakley S.B., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrell W.D., Butler A.P., Carter C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier B.E., Connor R., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhaun P.D., Dunn M.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graftham D.V., Griffiths C., Griffiths M.N.D., Guilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle B., Hunt A.R., Hunt S.B., Jenkins K., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaeisaiko M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McConachie L.J., McElroy K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Philimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Skuse C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wimling L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.";
 RL Nature 414:865-871 (2001).
 CC -!- SIMILARITY: Contains 2 ANK repeats.
 CC -!- SIMILARITY: Contains 1 ubiquitin-like domain.
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 DR EMBL; AU354776; CC17565.2; -

DR HSSP; P42771; 1DC2.
 DR Genew; HGNC:16117; C20orf86.
 DR InterPro; IPR02110; ANK.
 DR InterPro; IPR00626; Ubiquitin.
 DR PF0023; ankyrin.
 DR PRINTS; PRO1415; ANKIN.
 DR SMART; SM00248; ANK 2.
 DR PROSITE; PS50088; ANK REPEAT.
 DR PROSITE; PS50297; ANK REPEAT REGION; 1.
 DR PROSITE; PS00299; UBIQUITIN 1; FALSE NEG.
 DR PROSITE; PS50053; UBIQUITIN 2.
 DR PROSITE; PS50053; UBIQUITIN 2; 1.
 DR PROSITE; EC8B4A1414756CB CRC64;
 DR HYPOPOLETICAL PROTEIN; ANK repeat; REPEAT; POLYMORPHISM.
 DR DOMAIN 88 164 UBIQUITIN-LIKE.
 FT REPEAT 211 241 ANK 1.
 FT REPEAT 244 273 ANK 2.
 FT VARIANT 287 287 R -> C (in dbSNP:584855).
 SQ 1 RGPGRGAA|RASGPGGG 20
 Db 3 RAAAGGAGGARRAGPTGASR 22
 SEQUENCE 337 AA: 36714 MW; EC8B4A1414756CB CRC64;

RESULT 5
 A2AA_HUMAN STANDARD PRT; 450 AA.
 ID A2AA_HUMAN STANDARD PRT; 450 AA.
 AC P08913; Q9BZK1;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-2A adrenoreceptor (Alpha-2A adrenoreceptor) [Alpha-2AAR
 DE subtype C10].
 RA ADRA2A OR ADRA2R OR ADRA2.
 RA Homo sapiens (Human).
 OS Metzooa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Buteroidea; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1] _
 SEQUENCE FROM N.A.
 RN PDB FROM N.A.
 RN MEDLINE=89308571; PubMed=2568356;
 RX Fraser C.M., Arakawa S., McCombie W.R., Venter J.C.;
 RA Cloning, sequencing, and permanent expression of a human
 RA alpha-2-adrenoreceptor in Chinese hamster ovary cells. Evidence
 RA for independent pathways of receptor coupling to adenylylate cyclase
 RA attenuation and activation.".
 RA J. Biol. Chem. 264:11754-11761 (1989).
 RN [2] _
 SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RN TISSUE=Platelet;
 RX MEDLINE=9042789; PubMed=2823393;
 RA Kobilka B.K., Matsui H., Kobilka T.S., Yang-Peng T.L., Francke U.,
 RA Cloning, sequencing, and expression of the gene encoding the porcine
 RA alpha-2-adrenoreceptor. Allosteric modulation by Na⁺, H⁺, and
 RA amiloride analogs.
 RA J. Biol. Chem. 265:17307-17317 (1990).
 RN [4] _
 SEQUENCE FROM N.A.
 RA Castellano M., Giacche M., Rossi F., Rivadossi P., Perani C.,
 RA Beschi M., Agabiti Rosei E.;
 RA REVISIONS TO 333-365.
 RX MEDLINE=9100916; PubMed=2170371;
 RA Guyer C.A., Horstman D.A., Wilson A.L., Clark J.D., Kragoe E.J. Jr.,
 RA Limbird L.B.;
 RA "Cloning, sequencing, and expression of the gene encoding the porcine
 RA alpha-2-adrenoreceptor. Allosteric modulation by Na⁺, H⁺, and
 RA amiloride analogs."
 RA J. Biol. Chem. 265:17307-17317 (1990).
 RN [5] _
 SEQUENCE FROM N.A.
 RA Castellano M., Giacche M., Rossi F., Rivadossi P., Perani C.,
 RA Beschi M., Agabiti Rosei E.;

"A search for generic variability in the human alpha-2 adrenergic receptor on chromosome 10.";
Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
[5]

RP SEQUENCE FROM N.A., AND VARIANT LYS-251.
RX PMID:10566393; PubMed:10918191;
RA Small K.M.; Forbes S.L.; Brown K.M.; Liggett S.B.;
RT "An Asn to Lys polymorphism in the third intracellular loop of the human alpha 2A-adrenergic receptor imparts enhanced agonist-promoted Gi coupling.";
RT J. Biol. Chem. 275:38518-38523 (2000).
RL [6]

RQ SEQUENCE FROM N.A.
RA Mao Z.-M., Tang K., Li B.-M., Jing N.-H.;
RT "Cloning and expression of human alpha-2A adrenergic receptor in SY5Y cells.";
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL [7]

RQ SEQUENCE FROM N.A.
RA Liu L., Yuan L.;
RT "Human alpha-2A adrenergic receptor gene and the genotype of -1296 nucleotide and motionsickness.";
RT Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RL [8]

RP MUTAGENESIS OF PHE-412.
MEDLINE=91132079; PubMed:1678390;
RA Suryanarayana S.; Daunt D.A.; von Zastrow M.; Kobilka B.K.;
RT "A point mutation in the seventh hydrophobic domain of the alpha 2 adrenergic receptor increases its affinity for a family of beta receptor antagonists.";
RT J. Biol. Chem. 266:15488-15492 (1991).
RL [9]

RP MUTAGENESIS OF ASPARTIC ACID AND SERINE RESIDUES.
MEDLINE=911342598; PubMed:1673850;
RA Wang C.-D., Buck M.A., Fraser C.M.;
RT "Site-directed mutagenesis of alpha 2A-adrenergic receptors: identification of amino acids involved in ligand binding and receptor activation by agonists.";
RT Mol. Pharmacol. 40:168-179 (1991).
CC "ACTION: Alpha-2 adrenergic receptors mediate the catecholamine-induced inhibition of adenylyl cyclase through the action of G proteins. The rank order of potency for agonists of this receptor is oxymetazoline > clonidine > epinephrine > norepinephrine > phenylephrine > dopamine > p-synephrine > serotonin = p-octopamine. For antagonists the rank order is yohimbine > phenotolamine = mianserin > chloropromazine = spiperone = prazosin > dropananolol > alprenolol = pindolol.";
CC "-!- SUBCELLULAR LOCATION: Integral membrane protein.
CC "-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL; M23333; AAB5165.1; -.
DR EMBL; AAB5165; AAB5165.1; -.
DR EMBL; AF282016; ARG00447; -.
DR EMBL; AF281309; AAF91441; -.
DR EMBL; AF316894; AAK01634; -.
DR EMBL; AF284095; AAK26743; -.
DR EMBL; AY032736; AAK51162; -.
DR PIR; A34169; A34169.
PDB; 1HLL; 10-APR-02.
PDB; 1HO9; 24-JUL-02.
PDB; 1HOD; 24-JUL-02.
PDB; 1HOP; 24-JUL-02.
Genew; HGNC:281; ADRA2A.
MM; 104210; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004938; F:alpha2-adrenergic receptor activity; TAS.
DR GO; GO:0015559; P:potassium channel regulator activity; TAS.
DR GO; GO:0030016; P:actin cytoskeleton regulation and biogenesis; TAS.
DR GO; GO:0000628; P:cell motility; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. - .
DR GO; GO:0007194; P:negative regulation of adenylyl cyclase ac. - .
DR GO; GO:000884; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0007265; P:RAS protein signal transduction; TAS.
DR GO; GO:0007266; P:Rho protein signal transduction; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR00276; GPCR_Rhodopsin.
DR PR00001; Tm1; 1.
DR PRINTS; PS00237; G_PROMTIN_RECBP_FL1; 1.
DR PROSITE; PS00237; G_PROMTIN_RECBP_FL2; 1.
DR PROSITE; PS5052; G_Protein_RECBP; 1.
KW Multigene family; Phosphorylation; Lipoprotein; Glycoprotein;
KW Polymorphism; 3D-structure.
KW DOMAIN-1 33 59
FT TRANSMEM 1 34 59
FT DOMAIN 60 70
FT TRANSMEM 71 96
FT DOMAIN 97 106
FT TRANSMEM 107 129
FT DOMAIN 130 143
FT TRANSMEM 150 173
FT DOMAIN 174 192
FT TRANSMEM 193 217
FT DOMAIN 218 374
FT TRANSMEM 375 399
FT DOMAIN 400 406
FT TRANSMEM 407 430
FT DOMAIN 431 450
FT CARBOHYD 10 10
FT CARBOHYD 14 14
FT DISULFID 106 188
FT LIPID 442 442
FT SITE 113 113
FT SITE 200 200
FT SITE 204 204
FT VARIANT 251 251
FT MUTAGEN 79 79
FT MUTAGEN 113 113
FT MUTAGEN 130 130
FT MUTAGEN 200 200
FT MUTAGEN 204 204
FT MUTAGEN 333 365
FT CONFLICT 104 104
FT CONFLICT 157 157
FT CONFLICT 333 365
FT CONFLICT 368 368
SQ 450 AA; 48956 MW; A703CP26204BBAC CRC64;

Query Match Similarity 56.1%; Score 60; DB 1; Length 450;
 Best Local Similarity 63.6%; Pred. No. 7;
 Matches 14; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

FT DOMAIN 69 498 GLY-RICH.
 FT DOMAIN 499 613 ALA,GLY/PRO-RICH.
 FT SEQUENCE 721 AA: 742265 MN: 482C7A765C603B4A CRC64;

Query 1 RGPRGAGAARAS-GPGGGAPR 20
 Db 313 RGPRGKAKARASQVKEDSLPR 334

RESULT 6
 PUB2 RAT STANDARD; PRT; 721 AA.

AC Q99PF5;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DS Far upstream element binding protein 2 (FUSE binding protein 2) (KH protein 1) (MARTEL).
 DB protein splicing regulatory protein (KS9R) (MAP2 RNA trans-acting protein 1) (MARTEL).
 DE FUBP2 OR KHNSP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.
 RN [1] -Taxid=10116;
 RP SEQUENCE FROM N.A., SEQUENCE OF 73-87; 89-108 AND 475-486, SUBCELLULAR LOCATION, AND FUNCTION.
 RP TISSUE=Brain;
 RC MEDLNB=22246918; PubMed=12358951;
 RA Rehbein M., Weger K., Duck P., Schweizer M., Richter D., Kindler S.;
 RT "Molecular characterization of MARTEL, a protein interacting with the dendritic targeting element of MAP2 mRNA's."
 RL J. Neurochem. 82:1039-1046(2002).
 .-!- FUNCTION: Part of a ternary complex that binds to the downstream control sequence (DCS) of the pre-mRNA. Mediates exon inclusion in transcripts that are subject to tissue-specific alternative splicing. May interact with single-stranded DNA from the far-upstream element (FUSE). May activate gene expression (By similarity). Binds to the dendritic targeting element and may play a role in mRNA trafficking.
 CC -!- SUBUNIT: Part of a ternary complex containing FUBP2, PRBP1, PTBP2 and HNRPH (By similarity).
 CC -!- SUBCELLULAR LOCATION: Nuclear. A small proportion is also found in the cytoplasm of neuronal cell bodies and dendrites.
 CC -!- SIMILARITY: Contains 4 KH domains.

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 CC
 DR IM308818; AA039811.1; -.
 DR InterPro; IPR004087; KH_dom.
 DR InterPro; IPR004088; KH_type_1.
 DR SMART; SM00322; KH; 4.
 DR PROSITE; PS5004; KH_TYPE_1; 4.
 KW Transport; mRNA transport; mRNA processing; mRNA splicing;
 KW Transcript regulation; Trans-acting factor; Nuclear protein;
 KW DNA-binding; RNA-binding; Repeat.
 FT DOMAIN 145 209 KH 1.
 FT DOMAIN 234 300 KH 2.
 FT DOMAIN 323 387 KH 3.
 FT DOMAIN 425 492 KH 4.
 FT DOMAIN 572 685 4 X 12 AA IMPERFECT REPEATS.
 FT REPEAT 572 583 1.
 FT REPEAT 618 629 2.
 FT REPEAT 644 655 3.
 FT DOMAIN 674 685 4.
 FT DOMAIN 7 685 4.
 FT DOMAIN 7 685 4.

RESULT 7
 PUB2 RAT STANDARD; PRT; 1005 AA.

AC P54757;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ephrin type-A receptor 5 precursor (EGC 2.7.1.112) (Tyrosine-protein kinase receptor EK1) (EPH homology kinase-1).
 DE EPHAS OR EK1 OR EK-1.
 GN Rattus norvegicus (Rat).
 OS Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1] -
 RP SEQUENCE FROM N.A. (ISOFORM 1; 2; 3; 4 AND 5).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RC MEDLNB=9406777; PubMed=7504232;
 RA Maisonnierre P. C., Barrezueta N.X., Vancopoulos G.D.;
 RA "Ek1 and Ek-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression.";
 RA Oncogene 8:3277-3288(1993).
 RN [2] -
 RP SEQUENCE FROM N.A. (ISOFORM 6).
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RC MEDLNB=95205667; PubMed=78828646;
 RA Taylor V., Miescher G.C., Pfeaff S., Honegger P., Breitschopf H.,
 RA Lassmann H., Steck A.J.;
 RT "Expression and developmental regulation of Ekh-1, a neuronal Elk-like receptor tyrosine kinase in brain.";
 RL Neuroscience 63:163-178(1994).
 .-!- FUNCTION: Receptor for members of the ephrin-A family. Binds to ephrin-A1, -A2, -A3, -A4 and -A5.
 CC Name=1;
 CC -!- CATALYTIC ACTIVITY: ARP + a protein tyrosine = ADP + protein tyrosine phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: Named isoforms=6;
 CC Event=Alternative splicing; Named isoforms=6;
 CC IsoID=D54757-1; Sequence=Displayed;
 CC Name=2;
 CC IsoID=D54757-2; Sequence=VSP_003001;
 CC Name=3;
 CC IsoID=D54757-3; Sequence=VSP_003002;
 CC Name=4;
 CC IsoID=D54757-4; Sequence=VSP_003002; VSP_003003;
 CC Name=5;
 CC IsoID=D54757-5; Sequence=VSP_003001; VSP_003003;
 CC Name=6;
 CC IsoID=D54757-6; Sequence=VSP_003000; VSP_003002;
 CC -!- TISSUE SPECIFICITY: Almost exclusively expressed in the nervous system. Predominantly expressed in neurons.
 CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.
 CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
 CC -!- SIMILARITY: Belongs to the Tyr family of protein kinases. Ephrin receptor subfamily.
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CC EMBL; X78689; CAA53357.1; -.
 CC PIR; S49015; S49015.
 CC DR; S51603; S51603.
 CC HSSP; P00523; PTK.
 CC DR; InterPro; IPR006209; EGP like.
 CC DR; InterPro; IPR001030; Ephrin receptor.
 CC DR; InterPro; IPR009857; FN III-like.
 CC DR; InterPro; IPR003962; FnIII subd.
 CC DR; InterPro; IPR008979; Gal bind like.
 CC DR; InterPro; IPR000719; Proc_kinase.
 CC DR; InterPro; IPR001660; SAM.
 CC DR; InterPro; IPR001245; Tyr_Ptkinase.
 CC DR; InterPro; IPR008466; Tyr_Pkinase_AS.
 CC DR; InterPro; IPR001426; Ykase_receptor.
 CC PFam; PF00041; pfam00041.
 CC DR; PFam; PF00069; pfam00069.
 CC DR; PFam; PF00536; SAM; 1.
 CC DR; PRINTS; PR000014; FNTYPEBII.
 CC DR; PRINTS; PR00109; TYRKINASE.
 CC DR; ProDom; P0001495; Ephrin receptor; 1.
 CC DR; SMART; SMART00001; Protkinase; 1.
 CC DR; SMART; SMART00615; BPH_1bd; 1.
 CC DR; SMART; SMART00660; FNI; 2.
 CC DR; PROSITE; PS00219; TYRKc; 1.
 CC DR; PROSITE; PS00118; EGP_2; UNKNOWN_1.
 CC DR; PROSITE; PS00007; PROTEIN_KINASE_ATP; FALSE_NEG.
 CC DR; PROSITE; PS50001; PROTEIN_KINASE_DOM; 1.
 CC DR; PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 CC DR; PROSITE; PS00190; RECEPTOR_TYR_KIN_V_1; 1.
 CC DR; PROSITE; PS00191; RECEPTOR_TYR_KIN_V_2; 1.
 CC DR; PROSITE; PS50005; SAM_DOMAIN; 1.
 CC DR; Transfase; Transmembrane; Glycoprotein kinase; ATP-binding; Phosphorylation; Signal; Repeat; Alternative splicing.
 CC SIGNAL; 1.
 CC FT; CHAIN; 27.
 CC FT; DOMAIN; 27.
 CC FT; DOMAIN; 576.
 CC FT; DOMAIN; 597.
 CC FT; DOMAIN; 357.
 CC FT; DOMAIN; 467.
 CC FT; DOMAIN; 677.
 CC FT; DOMAIN; 967.
 CC FT; NP_BIND; 683.
 CC FT; BINDING; 709.
 CC FT; ACT_SITE; 802.
 CC FT; MOD_RBS; 652.
 CC FT; MOD_DES; 658.
 CC FT; MOD_RBS; 835.
 CC FT; MOD_RBS; 984.
 CC FT; CARBOHYD; 266.
 CC FT; CARBOHYD; 301.
 CC FT; CARBOHYD; 371.
 CC FT; CARBOHYD; 425.
 CC FT; CARBOHYD; 438.
 CC FT; CARBOHYD; 463.
 CC FT; VARSPLIC; 10.
 CC FT; VARSPLIC; 597.
 CC FT; VARSPLIC; 621.
 CC FT; CONFLICT; 170.
 CC FT; CONFLICT; 566.
 CC FT; CONFLICT; 578.
 CC FT; CONFLICT; 669.
 CC FT; CONFLICT; 708.
 CC FT; CONFLICT; 979.
 CC SQ; SEQUENCE; 1005 AA; 1110007 MN; 1A042C99693C574 CRC644;
 CC Query Match; 56.1%; Score 60; DB 1; Length 1005;
 CC Best Local Similarity; 61.9%; Pred. No. 14;
 CC Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;
 CC Qy; 2 GPRGAGGARASGGGG-APR 20
 CC Db; 5 GPRGAGGRRRTQGRGGGDTPR 25

RESULT 8
 COXB_HUMAN
 COXB_HUMAN STANDARD; PRT; 129 AA.
 AC P10606; Q96718.
 ID P10606; Q96718.
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Cytochrome c oxidase polypeptide VIb, mitochondrial precursor
 DE (EC 1.9.3.1).
 GN COX5B.
 OS Homo sapiens (Human).
 OC Bivalvia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88204368; PubMed=2840351;
 RA Zeviani M., Sakoda S., Superbary A., Nakase H., Rizzuto R.,
 RA Samitt C.E., Dinauro S., Schon E.A.;
 RT "Sequence of cDNAs encoding subunit VIb of human and bovine cytochrome
 C oxidase.";
 RL Gene 65:1-11(1998).
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91257815; PubMed=1646156;
 RA Lomax M.I., Hsieh C.L., Darras B.T., Francke U.;
 RT "Structure of the human cytochrome c oxidase subunit VIb gene and
 RT chromosomal mapping of the coding gene and of seven pseudogenes.";
 RL Genomics 10:1-9 (1991).
 RN RN
 RP SEQUENCE FROM N.A.
 RC TISSUE-SKIN; PubMed=12477932;
 RX
 RA Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow R.H., Schaefer C.P., Bhat N.K.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.P., Cassavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Carninci P., Prange C.,
 RA Raha S.S., Lognelliand N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guraratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
 RA Villalob D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E.,

RA Schein J.E., Jones S.J.M., Marra M.A.; Marra M.; Muridiae: Murinae: Mus.
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 PROC. NATL. ACAD. SCI. U.S.A. 99:16899-16903 (2002).
 [4]
 RN SEQUENCE OF 32-44.
 RP TISSUE=Liver;
 RC MEDLINE=94147969; PubMed=3133870;
 RX Hughes G.J., Prutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 Tissot J.-D., Bairoch A., Apel R.D., Hochstrasser D.F.;
 RT Human liver Protein map: update 1993.;
 Electrophoresis 14:1216-1222 (1993).
 CC -!- FUNCTION: This protein is one of the nuclear-coded polypeptide
 chains of cytochrome c oxidase, the terminal oxidase in
 mitochondrial electron transport.
 CC -!- CATALYTIC ACTIVITY: 4 ferricytochrome c + O(2) = 4 ferricytochrome
 c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: Belongs to the cytochrome c oxidase IVb family.
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 or send an email to license@isb-sib.ch).
 CC -!- EMBL; M59220; AAAS2060.1;
 DR EMBL; M19961; AAAS2061.1;
 DR EMBL; BC005229; AAH06229.1; -.
 DR PIR; J70324; OMIM5B
 DR SWISS-2DPAGE; P10606; HUMAN.
 DR Gene; HGNC:2269; COX5B.
 DR MIM; 123865; -.
 DR GO; GO:0004129; P:cytochrome-c oxidase activity; TAS.
 DR GO; GO:0007585; P:preprotein gaseous exchange; TAS.
 DR InterPro; IPR002124; COX5B.
 DR Pfam; PF01215; COX5B; 1.
 DR PROSITE; PS00848; COX5B; 1.
 KW Oxidoreductase; Inner membrane; Mitochondrion; Transit peptide;
 KW TRANSIT

FT CHAIN 32 129 CYTOCHROME C OXIDASE POLYPEPTIDE VB.
 FT METAL 91 91 ZINC (POTENTIAL).
 FT METAL 113 113 ZINC (POTENTIAL).
 FT METAL 116 116 ZINC (POTENTIAL).
 FT CONFFLICT 109 109 P -> Q (IN P. 1).
 SQ SEQUENCE 129 AA; 13695 MW; 8779F4CD34AC931 CRC64;
 FT TRANSIT 31 MITOCHONDRION.

Query Match 55.1%; Score 59; DB 1; Length 129;
 Best Local Similarity 57.9%; Pred. No. 3;
 Matches 11; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 RGPGRGAAARASGPGGGAP 19
 Db 20 RGPSGHAAAMRSMASGGCVP 38

RESULT 9

E2A5_MOUSE STANDARD; PRT; 877 AA.

AC Q60623;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ephrin type-A receptor 5 precursor (EC 2.7.1.112) (Tyrosine-protein

kinase receptor EPH-1) (EPH homology kinase-1) (Brain-specific kinase)

(CEK-7).

DE EPHA5 OR EHK1 OR CSK7 OR BSK.

GN EPHA5 OR EHK1 OR CSK7 OR BSK.

OS Mus musculus (Mouse);

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC

NCBI TaxID=10090;

[1]

SEQUENCE FROM N.A.

STRAN=BALB/C; TISSUE=Brain;

MEDLINE=94194501; PubMed=615300;

RA Zhou R.Y., Copeland T.D., Kromer L.F., Schulz N.T.;

RT "Isolation and characterization of Bsk, a growth factor receptor-like

tyrosine kinase associated with the limbic system.";

RT J. Neurosci. Res. 37:129-143 (1994).

CC -!- FUNCTION: Receptor for members of the ephrin-A family. Binds to

CC ephrin-A1, -A2, -A3, -A4 and -A5.

CC -!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein

tyrosine phosphate.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: BRAIN. IN EMBRYO, NON NEURONAL EXPRESSION

CC DOMAINS INCLUDE THE ECTODERM OF THE BRANCHIAL ARCHES, THE ECTODERM

AND MESENCHYME SURROUNDING THE DORSAL ROOT GANGLIA, THE

INTERVERTEBRAL DISKS, MAXILLARY AND MANDIBULAR MESENCHYMAL

ELEMENTS AS WELL AS THE NASAL MESENCHYME AND ECTODERM. WITHIN THE

DEVELOPING NERVOUS SYSTEM, ITS EXPRESSION IS VERY DYNAMIC. BESIDES

THE MIDBRAIN IT IS ALSO EXPRESSED IN THE HYPOTHALAMUS, AND THE

NEURHOYPOTHYSIS.

CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.

CC -!- SIMILARITY: Contains 1 fibronectin type III domain.

CC -!- SIMILARITY: Belongs to the tyr family of protein kinases. Ephrin

CC receptor subfamily.

CC -!- EMBL; U07357; AAA17038.1; -.

CC DR PIR; I48967; I48967.

CC DR HSSP; P2323; 1B47.

CC DR MGD; MG1:99654; Spisias.

CC DR InterPro; IPR06209; EGF like.

CC DR InterPro; IPR01090; Ephrin receptor.

CC DR InterPro; IPR01095; FN III-like.

CC DR InterPro; IPR03961; FN III.

CC DR InterPro; IPR003962; PT11 subd.

CC DR InterPro; IPR018919; GalBind-like.

CC DR InterPro; IPR007119; Prot_kinase.

CC DR InterPro; IPR001650; SAM.

CC DR InterPro; IPR01245; Tyr_kinase.

CC DR InterPro; IPR08266; Tyr_kinase AS.

CC DR InterPro; IPR001426; YKase receptor.

CC DR Pfam; PP01404; EPB1b6d, 1.

CC DR Pfam; PR00041; fna; 1.

CC DR Pfam; PR00069; pkinase; 1.

CC DR Pfam; PR00536; SAM; 1.

CC DR PRINTS; PR00014; FNTPIELI.

CC DR PRODOM; PD001495; Ephrin receptor; 1.

CC DR PRODOM; PD00001; Prot_kinase; 1.

CC DR SMART; SM00050; TN3; 1.

CC DR SMART; SM00454; SAM; 1.

CC DR SMART; SM00219; TyrK; 1.

CC DR PROSITE; PS01186; EGF 2; UNKNOWN 1.

CC DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

CC DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

CC DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V1; 1.

CC DR PROSITE; PS50791; RECEPTOR_TYR_KIN_V2; 1.

CC DR PROSITE; PS55105; SAM_DOMAIN; 1.

CC KW Transferase; Tyrosine-Protein kinase; ATP-binding; Phosphorylation;

CC KW Receptor; Transmembrane; Glycoprotein; Signal.

CC SIGNAL; 1 26 BY SIMILARITY.

CC FT

CC Wed Jun 23 16:19:17 2004

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman J., Madan A., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinwood J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.J., Skalska U., Smailus D.E.,
 RA Schnberk A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences";
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

-!- HETEROphilic interactions. In contrast to SCARF1, it poorly mediates the binding and degradation of acetylated low density lipoprotein (Ac-LDL) (By similarity).

CC SUBUNIT: Homophilic and heterophilic interaction via its extracellular domain. Interacts with SCARF1. The heterophilic interaction with SCARF1, which is stronger than the homophilic interaction with itself, is suppressed by the presence of SCARF1 ligand such as Ac-LDL (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -!- TISSUE SPECIFICITY: Predominantly expressed in endothelial cells. Expressed in heart, placenta, lung, kidney, spleen, small intestine and ovary.

CC -!- SIMILARITY: Contains 7 EGF-like domains.

CC -!- CAUTION: Ref-2 sequences differ from that shown due to frame-shifts in positions 750, 751 and 768.

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CC -!- EMBL: AF221996; AAN48861; -

DR EMBL; BC00054; AAH0054; ALT FRAME.
 DR EMBL; BC000926; AAH0926; ALT FRAME.

DR Genew; HGNC; 19869; SCARF2.

DR InterPro; IPR006219; EGF like.

DR InterPro; IPR006210; IEGF.

DR PRINTS; PR00011; EGF/EGFLAMININ.

DR SMART; SM00181; EGF; 7.

DR SMART; SM00180; EGF Lam; 6.

DR PROSITE; PS000022; EGF; 1; 7.

DR PROSITE; PS01186; EGF; 2; 4.

DR PROSITE; PS50026; EGF; 3; 3.

KW Cell adhesion; Receptor; Repeat; Signal; Transmembrane; BGF-like domain; Glycoprotein; Polymorphism.

KW SCAVENGER; RECEPTOR CLASS F MEMBER 2.

FT CHAIN 44 870 SIGNAL 1 43 SCAVENGER; RECEPTOR CLASS F MEMBER 2.

FT DOMAIN 44 441 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 442 462 POTENTIAL.

FT DOMAIN 463 830 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 76 110 EGF-LIKE 1.

FT DOMAIN 122 153 EGF-LIKE 2.

FT DOMAIN 154 182 EGF-LIKE 3.

FT DOMAIN 183 212 EGF-LIKE 4.

FT DOMAIN 213 241 EGF-LIKE 5.

FT DOMAIN 242 270 EGF-LIKE 6.

FT DOMAIN 372 403 EGF-LIKE 7.

FT DOMAIN 652 851 PRO-RICH.

FT DISULFID 80 92 POTENTIAL.

FT DISULFID 86 98 POTENTIAL.

FT DISULFID 100 109 POTENTIAL.

FT DISULFID 126 134 POTENTIAL.

FT DISULFID 128 142 POTENTIAL.

FT DISULFID 143 152 POTENTIAL.

FT DISULFID 156 163 POTENTIAL.

FT DISULFID 158 170 POTENTIAL.

FT DISULFID 181 193 POTENTIAL.

FT DISULFID 185 193 POTENTIAL.

FT DISULFID 187 200 POTENTIAL.

FT DISULFID 202 211 POTENTIAL.

FT DISULFID 215 222 POTENTIAL.

FT DISULFID 217 229 POTENTIAL.

FT DISULFID 231 240 POTENTIAL.

FT DISULFID 244 251 POTENTIAL.

FT DISULFID 246 258 POTENTIAL.

FT DISULFID 260 269 POTENTIAL.

FT DISULFID 376 384 POTENTIAL.

FT DISULFID 379 391 POTENTIAL.

FT DISULFID 393 402 N-LINKED (GLCNAC, -) (POTENTIAL).

FT CARBOHYD 83 83 N-LINKED (GLCNAC, -) (POTENTIAL).

FT CARBOHYD 310 310 N-LINKED (GLCNAC, -) (POTENTIAL).

FT CARBOHYD 365 365 N-LINKED (GLCNAC, -) (POTENTIAL).

FT CARBOHYD 403 403 N-LINKED (GLCNAC, -) (POTENTIAL).

FT VARIANT 777 777 D > E (IN dBSNP:759611).

FT VARIANT 778 778 /FTID=VAR 015148 V > L (IN dBSNP:759612).

FT VARIANT 819 819 /FTID=VAR 015149 A > G (IN dBSNP:874100).

FT VARIANT 837 837 /FTID=VAR 015150 A > G (IN dBSNP:874101).

FT VARIANT 777 777 /FTID=VAR 015151 MISSING (IN REF 2).

FT VARIANT 778 778 ALYARVGEARPARA > GTRPTTWITHSTADS (IN REF 2; AAH00584).

FT SEQENCE 870 AA; 92479 MW; DCB735A50E6B3D1P CRC64;

SQL

Query Match 53.3%; Score 57; DB 1; Length 870;
 Best Local Similarity 73.3%; Pred. No. 26;
 Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GPRGAGAARASGPGG 16
 Db 5 GPRGAGPARRGGAGG 19

RESULT 12

RLIB_XANAC STANDARD; PRT; 550 AA.

ID RLUB_XANAC ID Q8P388; PRT; 550 AA.

AC AC (Rel. 42, Created)

DT DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB DB Ribosoma1 large subunit Pseudouridine Synthase B (EC 4.2.1.70)

DE DE (Pseudouridylate synthase) (uracil hydrolyase).

GN GN RLUB OR XAC231B

OS OS Xanthomonas axonopodis (fp. citri).

OC OC Bacterium: Proteobacteria: Gammaproteobacteria: Xanthomonadales; Xanthomonadaceae: Xanthomonas.

NCBI_TaxID=9289; OC

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=306 / ATCC 13902 / XV 101;

RX MEDLINE=240215; PubMed=12024217;

RA RA Katsuyama A.M., Kishi L.T., Leite R.P., Reinhach F.C., Parach C.S., Purlan L.R.,

RA RA Quaggio R.B., Monteiro-Vitorelo C.B., Van Sluys M.A., Almeida N.F.,

RA RA Alves L.M.C., Co Amaral A.M., Berzolini M.C., Camargo L.F.A.,

RA RA Camarotte G., Cannava F., Cardozo J., Chambergo P., Ciapina L.P.,

RA RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA RA Pereira J.B., Pereira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA RA Formighieri E.F., Franco M.C., Gregorio C.C., Gruber A., Lemos M.V.F.,

RA RA Katsuyama A.M., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA RA Locali E.C., Machado M.A., Moraes L.M., Oliveira M.C., Oliveira V.R.,

RA RA Martins E.C., Meidanis J., Mouch C.P.M., Miyaki C.Y., Moon D.H.,

RA RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira R.P.,

RA RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.P.,

RA RA Spinola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,

RA RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.P.,

RA RA Setubal J.C., Kitajima J.P.,

RT RT Comparison of the genomes of two Xanthomonas pathogens with differing host specificities.;

elements.";
Nucleic Acids Res. 26:3542-3549 (1998).
 [12]

INTERACTION WITH SRS12;
 MEDLINE=200221511; PubMed=10757789;

RT Barnard D. C.; Factor J. G.;
RT "Identification and characterization of a novel serine-arginine-rich
 splicing regulatory protein.";
RT Mol. Cell. Biol. 20:3049-3057(2000).

CC FUNCTION: Plays a role in preventing exon skipping, ensuring the
 accuracy of splicing and regulating alternative splicing.
 Interacts with other spliceosomal components, via the RS domains,
 to form a bridge between the 5' and 3' splice site binding
 components, U1 snRNP and U2AF. Can stimulate binding of U1 snRNP
 to a 5'-splice-site-containing pre-mRNA. Binds to purine-rich RNA
 sequences, either the octamer, 5'-RGAAGAC-3', (rA or G) or the
 decamers, AGGAGAGC/AGGCAAGC. Three copies of the octamer
 constitute a powerful splicing enhancer in vitro, the ASF/SF2
 dependent splicing. Isoform ASF-2 and isoform ASF-3 act as
 splicing repressors.

CC SUBUNIT: Consists of two polypeptides of P32 and P33. In vitro,
 binds SRS11 (ASF/SF2), SRS70 and U2AF1 but not U2AF2. Binds
 SRS12. Interacts with SRS70/SAP1.

CC SUBCELLULAR LOCATION: Nuclear.

CC ALTERNATIVE PRODUCTS: Named isoforms=3;

Event=Alternative splicing; Named isoforms=3;

Name=ASF-1;

Isold=Q01955-1; Sequence=Displayed;

CC Name=ASF-2;

Isold=Q01955-2; Sequence=VS2_0005836;

CC Isold=Q01955-3; Sequence=VSP_005837; VSP_005858;

CC PTM: Extensively phosphorylated on serine residues in the RS
 domain.

CC SIMILARITY: Belongs to the splicing factor SR family.

CC -!- SIMILARITY: Contains 2 RNA recognition motif (RRM) domains.

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CC EMBL: M6940; AAA03476.1; -.
 EMBL: M72709; AAA3565.1; -.

DR MIM: 600812; -.

DR GO: GO:0008248; P:pre-mRNA splicing factor activity; TAS.

DR GO: GO:0006397; P:mRNA processing; TAS.

DR InterPro; IPR000504; RNA_rec_mot.

DR SMART; SM00360; RRM; 2.

DR PROSITE; PS50102; RRM; 2.

DR PROSITE; PS00030; RRM_RNP_1; FALSE NEG.

KW mRNA processing; mRNA_splicing; Nuclear protein; RNA-binding.

KW Repeat; Alternative splicing; Acetylation; Phosphorylation.

KW INIT_MET 0 0 RNA-BINDING (RRM) 1.

PT DOMAIN 15 90 RNA-BINDING (RRM) 2.

PT DOMAIN 120 194 Gly-Rich (Hinge region).

PT DOMAIN 93 112 Arg/Ser-Rich (RS DOMAIN).

PT DOMAIN 197 246 Interacts with SRS11.

PT DOMAIN 246 Interacts with SRS12.

CC SEQUENCE FROM N.A.
 STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 MEDLINE=2147740; PubMed=11572948;

RA Omura S.; Ikeda H.; Ishikawa J.; Hanamoto A.; Takahashi C.,
 Shinose M.; Takahashi Y.; Nakazawa H.; Osonee T.,
 Kikuchi H.; Shiba T.; Sakai Y.; Hattori M.;
 Streptomyces avermitilis. *Bacteriaceae; Actinomycetidae; Actinomycetes;*
 Streptomyces; Streptomyctaceae; Streptomyces. NCBI_TAXID=33901;

RA [1]

RN SEQUENCE FROM N.A.
 STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;
 MEDLINE=22608306; PubMed=12695562;

RA Ikeda H.; Ishikawa H.; Hanamoto A.; Omura S.;
 Sakai Y.; Hattori M.; Omura S.;
 "Complete genome sequence and comparative analysis of the industrial
 microorganism *Streptomyces avermitilis*."; RL Biotechnol. 21:526-531(2003).

RT FUNCTION: One of the essential components for the initiation of
 protein synthesis. Protects formimino-tRNA from spontaneous
 hydrolysis and promotes its binding to the 30S ribosomal subunits.
 Also involved in the hydrolysis of GTP during the formation of the
 70S ribosomal complex (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic.

CC -!- SIMILARITY: Belongs to the IP-2 family.

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CC RX MEDLINV=94018366; PubMed=8412494;
 CC RA Blaxall H.S.; Heck D.A.; Bylund D.B.;
 CC RT "Molecular determinants of the alpha-2D adrenergic receptor subtype.";
 CC RL Life Sci 53:9-9 (1993).
 CC -!- FUNCTION: Alpha-2 adrenergic receptors mediate the catecholamine-induced inhibition of adenylyl cyclase through the action of G proteins.
 CC SUBCELLULAR LOCATION: Integral membrane protein.
 CC TISSUE SPECIFICITY: Retina, brain and olfactory lobe.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL: U79030; AAC24581; -;
 CC EMBL: S66295; AAB28450.1; -;
 CC PIR: I46958; I46558.
 CC HSSP: P2924; 1 MMH.
 CC InterPro: IPR00276; GPCR_Rhodopsn.
 CC DR InterPro: IPR00276; GPCR_Rhodopsn.
 CC DR Pfam: PF00001; 7tm1; 1.
 CC DR PRINTS: PR0023; GPCR_RHODOPSN.
 CC DR PROSITE: PS00271; G-PROTEIN RECEPTOR_F1_1.
 CC DR PROSITE; PS00272; G-PROTEIN RECEPTOR_F1_2; 1.
 CC DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 CC KW Multigene family; Phosphorylation; Lipoprotein; Palmitate.
 CC FT DOMAIN 1 33 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 2 59 1 (POTENTIAL).
 CC FT DOMAIN 60 59 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 71 2 (POTENTIAL).
 CC FT DOMAIN 97 96 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 107 106 3 (POTENTIAL).
 CC FT DOMAIN 130 129 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 150 149 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 173 173 4 (POTENTIAL).
 CC FT DOMAIN 192 192 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 193 193 5 (POTENTIAL).
 CC FT DOMAIN 218 376 CYTOPLASMIC (POTENTIAL).
 CC FT DOMAIN 327 401 6 (POTENTIAL).
 CC FT DOMAIN 402 411 EXTRACELLULAR (POTENTIAL).
 CC FT DOMAIN 412 432 7 (POTENTIAL).
 CC FT DOMAIN 433 452 CYTOPLASMIC (POTENTIAL).
 CC FT CARBOHYD 10 10 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 14 14 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT DISUPTD 1046 188 BY SIMILARITY.
 CC FT LIPID 444 444 S-palmitoyl cysteine (By similarity).
 CC SQ SEQUENCE 452 AA; 49252 MW; F1001DD2860CD8F9 CRC64;
 CC
 CC Query Match 50.5%; Score 54; DB 1; Length 452;
 CC Best Local Similarity 59.1%; Pred. No. 31;
 CC Matches 13; Conservative 0; Mismatches 2; Gaps 1;
 CC
 CC Qy 1 RGPPIGAGAARASGGGGGAR 20
 CC Db 328 RGPPIGGG--RPGGPGGGGR 345
 CC
 CC RESULT 15
 CC A2AA_BOVIN STANDARD; PRT; 452 AA.
 CC ID A2AA_BOVIN
 CC AC Q258738;
 CC DT 16-OCT-2001 (Rel. 40, Created)
 CC DT 16-OCT-2001 (Rel. 40, Last sequence update)
 CC DT 15-MAR-2004 (Rel. 43, Last annotation update)
 CC DE Alpha-2A adrenergic receptor (Alpha-2A adrenoreceptor) (Alpha-2AAR)
 CC DE (Alpha-2D adrenergic receptor) (Alpha-2D adrenoreceptor) (Alpha-2DAR)
 CC GN ADR2A.
 CC OS Bos taurus (Bovine).
 CC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC OC Bovidae; Bovinae; Bos.
 CC OX NCBI_TaxID=9913;
 CC RN [1]
 CC SEQUENCE FROM N.A.
 CC MEDLINV=9411113; PubMed=9450652;
 CC RX Duda T.; Sharma R.K.; Venkateswaran V.
 CC RT "The bovine alpha-2D-adrenergic receptor gene: structure, expression in retina, and pharmacological characterization of the encoded receptor";
 CC RT Mol. Cell. Biochem. 177:113-123 (1997).
 CC RN [2]
 CC SEQUENCE OF 171-210 FROM N.A.
 CC
 CC Search completed: June 22, 2004, 08:51:57
 CC Job time : 16 sec/s

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OM Protein - protein search, using sw model

Run on: June 22, 2004, 08:47:17 ; Search time 48 Seconds
(without alignments)

131.466 Million cell updates/sec

Title: US-09-529-206D-4_COPY_43_62

Perfect score: 107

Sequence: 1 RGPGRGAAARASPGGGAPR 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_recom:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_rvirus:*

16: sp_bacteriopl:*

17: sp_archeap:*

17 58 54.2 775 16 Q9PF42 streptomyce

18 57 53.3 129 11 Q9dB81 mus musculus

19 57 53.3 355 16 Q9W009 streptomyce

20 57 53.3 412 5 Q960D3 drosophila

21 57 53.3 2 Q8KUG4 actinomycete

22 57 53.3 443 5 Q9VBA3 drosophila

23 57 53.3 457 10 Q941k1 oryza sativa

24 57 53.3 853 2 Q8VQZ0 myxococcus

25 57 53.3 857 2 Q85783 myxococcus

26 57 53.3 866 4 Q8IXP3 homosapien

27 56 52.3 158 11 Q8C292 mus musculus

28 56 52.3 200 10 Q8WFA2 homosapien

29 56 52.3 256 4 Q96ME8

30 56 52.3 478 16 Q82F52 streptomyce

31 56 52.3 520 10 Q7XLJ7 oryza sativa

32 56 52.3 559 10 Q8L680 oryza sativa

33 56 52.3 730 10 Q7XTS8 oryza sativa

34 56 52.3 867 10 Q94LJ1 oryza sativa

35 56 52.3 887 10 Q9FF4 oryza sativa

36 56 52.3 894 10 Q7X870 oryza sativa

37 56 52.3 921 10 Q9FMC5

38 56 52.3 921 10 Q7XCP6

39 56 52.3 953 10 Q8LJB9

40 56 52.3 968 10 Q7XTU9

41 56 52.3 1029 10 Q7SX7 oryza sativa

42 56 52.3 1030 10 Q7XWA8 oryza sativa

43 56 52.3 1033 10 Q81AJ5

44 56 52.3 1033 10 Q7XVS0

45 56 52.3 1035 10 Q8LICB

ALIGNMENTS

RESULT 1									
ID		Q9NY13		PRELIMINARY;		PPR;		142 AA.	
AC		Q9NY13;		Q9NY13;		Q9NY13;		Q9NY13;	
DT		01-OCT-2000		(TREMBLrel. 15, Created)		(TREMBLrel. 15, Last sequence update)		(TREMBLrel. 15, Last annotation update)	
DR		DT		DT		DT		DT	
KW		Hypothetical protein.		Hypothetical protein (Fragment).		Hypothetical protein.		Hypothetical protein.	
FT		LAGE_2.		LAGE_2.		LAGE_2.		LAGE_2.	
GN		Homo sapiens (Human).							
OS		Bukaryote; Metazoa; Chordates; Craniata; Vertebrata; Butteleostomi;							
OC		Mammalia; Butheroidea; Primates; Catarrhini; Hominidae; Homo.							
RN		[1]		[1]		[1]		[1]	
RP		SEQUENCNCB FROM N.A.							
RA		Lethe B.G;		Lethe B.G;		Lethe B.G;		Lethe B.G;	
RL		Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.							
DR		DR		DR		DR		DR	
EMBL		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR		DR		DR	
EMB		DR		DR					

GN LAGE1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates;
 OC Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RRP TISSUE=Placenta;
 RRC MEDLINE=9932550; PubMed=10399963;
 RRA "Arribalzaga C.A., Van den Doel P.B., Heemskerk B., Schrier P.I.;
 RRA "interleukin-2-induced, melanoma-specific T cells recognize CAMEL, an
 RRT "unexpected translation product of LAGE-1.";
 RRL Int. J. Cancer 82:442-448 (1999).
 RRN [2]
 SEQUENCE FROM N.A.
 RRA Aradhya S., Bardaro T., Galgoczy P., Yamagata T., Esposito T.,
 RRA Patil H., Ciccodicola A., Kenrick S., Platzter M., D'Urso M.,
 RRA Nelson D.L.;
 RRA "Multiple pathogenic and benign genomic rearrangements occur at a 35-
 RRT kb duplication involving the NEMO and the LAGE2 genes.";
 RRL Hum. Mol. Genet. 0:0-0(2001).
 EMBL: A012834; CAA10194; 1;
 DDBJ AF227315; AAB12015; 1;
 DQR SEQUENCE 180 AA; 18236 MW; 9077FAF953543A25 CRC64;
 SEQUENCE 180 AA; 18236 MW; 9077FAF953543A25 CRC64;
 SEQUENCE FROM N.A.
 Q9BB80 PRELIMINARY;
 ID Q9BB80 PRT: 210 AA.
 AC ACID_01-FUN-2001 (TREMBLrel. 17, Created)
 DT 01-FUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DB Cancer/testis antigen 2.
 DB Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Mammalia; Eutheria; Primates;
 OC Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 [1]
 RN SEQUENCE FROM N.A.
 RRP TISSUE=Placenta;
 RRA Strausberg R.;
 RRL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 EMBL: BC002833; AAH02833; 1;-
 DQR SEQUENCE 210 AA; 210089 MW; BFB5BF04FB04E8BE CRC64;
 SEQUENCE 210 AA; 210089 MW; BFB5BF04FB04E8BE CRC64;
 SEQUENCE FROM N.A.
 Q9UB80 PRELIMINARY;
 ID Q9UB80 PRT: 210 AA.
 AC ACID_01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DB LAGE-1L protein.
 DQR SEQUENCE FROM N.A.
 Q9UB89 PRELIMINARY;
 ID Q9UB89 PRT: 210 AA.
 AC ACID_01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DB LAGE-1L protein.
 DQR SEQUENCE FROM N.A.
 Q9UB90 PRELIMINARY;
 ID Q9UB90 PRT: 210 AA.
 AC ACID_01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DB LAGE-1L protein.

OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID=9606;
RN	
RC	SEQUENCE FROM N.A.
TISSUE	=Melanoma;
RX	MEDLINE=99325550; PubMed=10399963;
RA	Aarnoudse C.A., 'Van den P.B., Heemskerk B.; Schrier P.I.;
RT	"Interleukin-2-induced, melanoma-specific T cells recognize CAMEL unexpected translatant product of LAGE-1.";
RT	Int. J. Cancer 62:44-48 (1999).
DR	EMBL: AJ012835; CAA10196.1; -.
SQ	SEQUENCE 210 AA; 21060 MN; 1DD0B1029735B60A CRC64;
Query Match	92.5%; Score 99; DB 4; Length 210;
Best Local Similarity	95.0%; Pred. No. 0.00015;
Matches 19;	Conservative 0; Mismatches 1; Indels 0; G
Qy	1 RGPGRGAAARASGPCCGAPR 20
Db	43 RGPGRGAAARASGPCCGAPR 62
RESULT 5	
Q8WSZ3	PRELIMINARY; PRT; 301 AA.
ID	Q8WSZ3
AC	Q8WSZ3;
DT	01-MAR-2002 (TREMBLrel. 20, Created)
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DB	Dragonfly silk protein spidroin 2 (Fragment).
OS	Nephila clavata (Joro spider).
OC	Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae; Aranomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.
OC	NCBI_TaxID=70342;
RN	
RP	SEQUENCE FROM N.A.
RA	Ma H.W., Zhang L.S., Lu Y.M., Liu Z.S., Zhang Y.J.;
RT	"Amplification, Cloning and Sequence Analysis of Spider Dragline CDNA."
RT	Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
RL	EMBL: AF441245; AAL32472.1; -.
DR	NON_TER 1
FT	NON_TER 1
SQ	SEQUENCE 301 AA; 25396 MN; BC69428B56843D74 CRC64;
Query Match	57.9%; Score 62; DB 5; Length 301;
Best Local Similarity	66.7%; Pred. No. 6.1;
Matches 12;	Conservative 1; Mismatches 5; Indels 0; G
Qy	2 GPRGAGAAARASGPCCGAP 19
Db	130 GPGGAAAAAAGPGGAGP 147
RESULT 6	
Q86P11	PRELIMINARY; PRT; 550 AA.
ID	Q86P11
AC	Q86P11;
DT	01-JUN-2003 (TREMBLrel. 24, Created)
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DB	J1p2.
OS	Toxoplasma gondii.
OC	Bukaryota; Alveolata; Ciliophora; Bimerida; Sarcocyst Toxoplasma.
OC	NCBI_TaxID=5811;
RN	
RP	SEQUENCE FROM N.A.
STRAN	=RH;
RA	Jiang L., Shu H., Luo S., Wu X., Cai L., Wang D., Zeng Q.;
RT	"Immunological screening of Toxoplasma tachyzoite cDNA libraries with serum from toxoplasma infected rats."

RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY208675; AAC043429.1; -;
 SQ SEQUENCE 550 AA; 57890 MW; 18C71B4974BF0F34 CRC64;

Query Match Score 62; DB 5; Length 550;
 Best Local Similarity 63.2%; Pred. No. 11;
 Matches 12; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 Qy 2 GPRGAGAARASGPGGGAPR 20
 Db 524 GFORAGRAQADGIGAGPR 542

RESULT 7
 Q8S0W4 PRELIMINARY; PRT; 1039 AA.
 ID Q8S0W4
 AC Q8S0W4
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DT QJ1014_G12.10 protein.
 D3 QJ1014_G12.10
 OS Oryza sativa (Japonica cultivar-group)
 OC Bokaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; Liliopsida; Poaceae;
 OC Bhrhartoideae; Oryzeae; Oryza.
 OX NCBI_TaxID:39947;

RN SEQUENCE FROM N.A.
 RC Nipponbare;
 RA Sasaki T., Matsumoto T., Yamamoto K.;
 RT "Oryza sativa (Japonica cultivar-group) genomic DNA, chromosome 1, BAC
 clone:QJ1014_G12.";
 RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 *RL EMBL: AAC03372; BAB83076.1; -.
 DR Gramene; Q8S0W4; -;
 DR InterPro; IPR007228; DUF390.
 DR InterPro; IPR007321; Transposase_...
 DR Pfam; PP04394; DUF390.1.
 DR Pfam; PP04395; Transposase_28; 1.
 SQ SEQUENCE 1039 AA; 11263 MW; A9A60FD348755DFD CRC64;

Query Match Score 62; DB 10; Length 1039;
 Best Local Similarity 73.7%; Pred. No. 19;
 Matches 14; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 3 PAGAGAARASG--PGGGAP 19
 Db 363 PGGGAAARASRPGGGAP 381

RESULT 8
 Q9BIT7 PRELIMINARY; PRT; 1953 AA.
 ID Q9BIT7
 AC Q9BIT7
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DT Major ampullate spiderin 2-like protein (Fragment).
 DE Nephila inaurata madagascariensis.
 OS Nephila inaurata madagascariensis.
 OC Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.
 OC NCBITaxID:115969;
 RN [1] SEQUENCE FROM N.A.
 RP MEDLINE=21119804; PubMed=11283372;
 RA Gatesy J., Hayashi C., Motriuk D., Woods J., Lewis R.;
 RT "Extensive Diversities, Conservation, and Convergence of Spider Silk
 Fibroin Sequences";
 RL Science 291:2603-2605 (2001).
 EMBL; AF350276; AAK30605.1; -.
 FT NON_TER 1 1
 FT NON_TER 1953 1953

RESULT 9
 Q86TH8 PRELIMINARY; PRT; 465 AA.
 ID Q86TH8
 AC Q86TH8
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DB Adrenergic, alpha-2A-, receptor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBITaxID:9606;
 RN [1] SEQUENCE FROM N.A.
 RC TISSUE=Peripheral Nervous System;
 RA Straubberg R.;
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC050414; AH50414.1; -.
 DR GO:0016021; C: integral to membrane; IEA.
 DR GO:0004872; P: receptor activity; IEA.
 DR GO:0001584; P: rhodopsin-like receptor activity; IEA.
 DR GO:0007186; P: G-protein coupled receptor protein signalin. . ; IEA.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1_1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_Protein_RECBP_F1_1;
 DR PROSITE; PS50262; G_Protein_RECBP_F1_2;
 KW Receptor.
 SQ SEQUENCE 465 AA; 50646 MW; 58-E576149BDB696 CRC64;

Query Match Score 60; DB 4; Length 465;
 Best Local Similarity 63.6%; Pred. No. 16;
 Matches 14; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 1 RGPRGAGAARAS--GPGGGAPR 20

Db 328 RGPRGKKGKARASQVRPGDSLPR 349

RESULT 10
 Q8R554 PRELIMINARY; PRT; 926 AA.
 ID Q8R554
 AC Q8R554
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DB Cezanne 2 protein.
 GN AJ430384 OR CZEZANNE 2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBITaxID:10090;
 RN [1] SEQUENCE FROM N.A.
 RC STRAIN=C57 BL/6;
 RA Evans P.C., Cadwell W.J., Kilshaw P.J.;
 RT "Isolation of a novel murine gene, Cezanne 2, ";
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 EMBL; AJ410384; CAD23048.1; -.
 DR MGI; MGI:2158505; AJ430384.
 DR InterPro; IPR003323; OTU; 1.
 DR PROSITE; PS50802; OTU; 1.

SEQUENCE FROM N.A. PubMed=9851916;

DR InterPro; IPR01426; YKase-receptor.

DR DR PFM; PF0104; EPH_lbd; 1.

DR PFM; PF00041; Fn3; 2.

DR PRINTS; PR00014; FNTRPEIII.

DR PRODom; P00014; EPH_lbd.

DR SMART; SM00615; EPH_lbd; 1.

DR SMART; SM00060; Fn3; 2.

DR PROSITE; PS01186; EGF_2; 1.

DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V1; 1.

DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V2; 1.

DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V2; 1.

SEQUENCE 681 AA; 75336 MW; 92B9187AB78BB722 CRC64;

Query Match 55.1%; Score 59; DB 11; Length 681; Best Local Similarity 61.9%; Pred. No. 30; Matches 13; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

Qy 2 GPRGAGARASGPGGG~APR 20

Db 5 GPRGAGHRRRTQRGGGDDTPR 25

RESULT 14

Q9BITS ID Q9BITS PRELIMINARY; PRT; 563 AA.

AC AC Q9BITS; DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DE DE Major ampullate spidroin 2 (Fragment).

GN MASP2.

OS Nephila inaurata madagascariensis.

OC Eukaryota; Metazoa; Arthropoda; Cheliceraata; Arachnida; Araneae; Araneomorphae; Entelegynae; Araneoidea; Tetragnathidae; Nephila.

NCBI_TaxID=115969;

RN [1]

RP SEQUENCE FROM N.A. PubMed=2179804; PubMed=1128372;

RA Gatesy J., Hayashi C., Morriuk D., Woods J., Lewis R.; RT "Extreme Diversity, Conservation, and Convergence of Spider Silk Ribron Sequences." *Science* 291:2603-2605(2001).

RL EMBL; AF30278; AAC06071; -.

FT NON-TER 1

FT NON-TER 1

FT NON-TER 1

SQ SEQUENCE 563 AA; 48361 MW; QAEAD885304B886B CRC64;

Query Match 54.7%; Score 58.5; DB 5; Length 563; Best Local Similarity 59.1%; Pred. No. 29; Matches 13; Conservative 2; Mismatches 4; Indels 3; Gaps 1;

Qy 1 FGPRGAG---AARASGPGGAP 19

Db 406 QGPGGAGSAAAAAAGPGGCGP 427

RESULT 15

Q19581 ID Q19581 PRELIMINARY; PRT; 566 AA.

AC AC Q19581; DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

GN F18H3.3B Protein.

OS Caenorhabditis elegans.

OS Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peleodinae; Caenorhabditis.

NCBI_TaxID=6239;

RN [1]

RP SEQUENCE FROM N.A. PubMed=119951 to the EMBL/GenBank/DBJ databases

RT Submitted; Coles L.; RA